Appli Appli

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

Result No.

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Sequence 1, Ap
Sequence 2, Ap
Sequence 2, Ap
Sequence 2, Ap
Sequence 10, A
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08729103
Sequence 1, Application US/08729103
Sequence 1, Application US/08729103
Sequence 1, Application US/08729103
SEREMAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
ITILE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 314 Porter Drive
CITY: Palo Alco
STATE: CA
COUNTY: US
ITY: PALO Alco
STATE: CA
COUNTY: US
ITY: BAJOALE FORM:
MEDIUM TYPE: Diskette
                                US-07-893-929A-5
PCT-US92-10344-5
US-07-893-10344-5
PCT-US92-10344-2
US-07-893-929A-3
PCT-US92-10344-3
US-07-893-929A-1
PCT-US92-10344-1
PCT-US92-10344-1
PCT-US92-10344-1
US-08-709-662-2
US-08-708-68-34-10
US-09-111-470-10
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COMPUTER: BACCOMPALIDLE
COMPUTER: IBM COMPALIDLE
SOFTWARE: FASTEN DGS
SOFTWARE: FASTEN DGS
SOFTWARE: FASTEN DGS
SOFTWARE: FASTEN DGS
FILING DATE: FILED HETWICH
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FILED HETWICH
APPLICATION NUMBER:
FILING DATE:
FILIN
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLNFET02
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US-08-729-103-1
US-08-729-103-1
    204
1198.5
1198.5
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1198.5
1198.5
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1190
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1189
1189
    Patent No. 5514582
Sequence 2, Appli
                                                                                                                                                                                                                                                     December 31, 2003, 09:11:17 ; Search time 41 Seconds (without alignments) 163.052 Million cell updates/sec
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878
1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
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Sequence 7, 1
Sequence 7, 1
Sequence 1, 1
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                    version 5.1.6
- 2003 Compugen Ltd.
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US-08-468-413-2

US-08-468-413-2

US-08-70169-2

US-08-701-103-3

US-08-709-103-3

US-08-709-662-7

US-08-709-662-5

US-08-709-662-5

US-08-709-662-5

US-08-709-662-5

US-08-709-662-5

US-08-709-662-5

US-08-709-662-6

US-08-709-608-6

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US-08-709-662-3
US-07-893-929A-7
PCT-US92-10344-7
US-08-822-261-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                    GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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Gaps

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FILING DATE:
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                     RESULT 3
US-09-162-508-2
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                                                                                                   61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                   61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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MASRSMRLLLLLSCLAKTGVLGDI IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                             MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MASRSMRLLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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Best Local Similarity 100.0%; Pred. No. 2e-88;
Matches 158; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSWGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                      121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                         121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08468413
Patent No. 5861494
GENERAL INFORMATION:
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WORD PERPECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,413
FILING DATE: 06 JUN 95
CLASSIFICATION: 435
APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325800-447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 35.134
FREFRENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i: 158 AMINO ACIDS
AMINO ACID
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TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07068
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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Best Local Similarity 100.0%; Pred. No. 2e-88;
Matches 158; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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                                            GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9507169
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/468,413
PILING DATE: 06 JUN 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
Sequence 2, Application US/09162508
Patent No. 6080722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1701
TELEPAX: 201-994-1701
TELEPAX: 201-994-1702
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                            CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: LINEAR
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52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RLLLLLSCLAKTGVLGDIIMRPS------CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-20;
es 51; Indels
    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-729-103-3
Sequence 3, Application US/08729103
Fatent No. 5837841
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%; Score 254.5; 30.6%; Pred. No. 3.5
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SOFTWARE: FASTESEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 0057;
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-929
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                 : 165 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.6%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-401-530A-7
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MASRSMRILLLISCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 878; DB 5 Best Local Similarity 100.0%; Pred. No. 2e-88; Matches 158; Conservative 0; Mismatches
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07169
FILING DATE: 06 JUN 95
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEB: Banner & Allegretti
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,134
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAID:
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 158 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-1895-07169-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner &
ROSELAND
NEW JERSEY
                                         USA
                                                               07068
                                         COUNTRY:
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52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
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                                                                                                                          --- CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                 5 KYFILLSCL-----MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGY
                                                                               Gaps
                                                                                                                                                                                                                                                                                                  110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                                                                                                                                           29;
                                     Length 165;
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                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Score 240; DB 2; 34.3%; Pred. No. 1.3e-18; tive 27; Mismatches 57
                                 Query Match 29.0%; Score 254.5; DB 2
Best Local Similarity 30.6%; Pred. No. 3.5e-20;
Matches 52; Conservative 38; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                          7 RLLLLSCLAKTGVLGDIIMRPS-
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; Sequence 4, Application US/08729103-
; Patent No. 5837841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 166 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 46; Conserv
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
US-08-709-662-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-729-103-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                                                     S KYFILLSCL------WULSPSQQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW
                                                                                                                                                                                                                                                                                                                                            ---CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                                                                                                                                                  Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                        DB 2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vinik, Aaron I.
APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rascanberg, Lawrence
APPLICANT: Nogenberg, Lawrence
APPLICANT: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                            3.5e-20
                                                                                                                                                                                                                                                      Query Match
29.0%; Score 254.5; Dest Local Similarity 30.6%; Pred. No. 3.5e-Matches 52; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: US
COUNTY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                            7 RLLLLSCLAKTGVLGDIIMRPS
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Patent No. 5840531
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1001 G Street, N.W CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-500-521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acids
               SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                       MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                    LIBRARY: GenBank
CLONE: 393209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                              US-08-729-103-3
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Matches
87 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSS 143
                         3 STDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGPKKWKD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 ELEÇQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 26.3%; Score 231; DB 2; Length 174; I Similarity 32.4%; Pred. No. 1.4e-17; 55; Conservative 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                            APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PFILING DATE: US/08/401,530A
FILING DATE: 25-FEB-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                 Sequence 5, Application US/08401530A
Patent No. 5834590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1001 G Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 5:
                                                                             144 NECNKRQHFLCKYR 157
                                                                                                      | |: |:||::
152 ESCEKKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 174 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 55; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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55 ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 DLACQKRPSG-HLVSVLSGSEASFVSSLIKSSGNSGQNVWIGLHDPTLGQEPNRGGWEWS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VALTIMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALPSVSKSWPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73; Indels 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Dujuid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pittenger, Gary L.
APPLICANT: Refaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Daylid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 231; DB 2;
Pred. No. 1.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/709,662
09-SEP-1996
                                                                                                                                                                                                                                                                               ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
Application US/08709662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 005
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-401-530A-6
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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64

RESULT 10

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,1
  Floppy disk
                                                                                                                                                                                                                                                                                  TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 41; Conserv
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; Patent No. 5514582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 VNNNQDIWIMLHDPTWGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
    APPLICANT: Vinik, Aaron I.
    APPLICANT: Pittenger, Gary L.
    APPLICANT: Rafaeloff, Ronit
    APPLICANT: Rosenberg, Lawrence
    APPLICANT: Duguid, William P.
    TITLE OF INVENTION: ISLET NEOGENESIS
    NUMBER OF SEQUENCES:
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Score 228.5; DB 2; Length 174; illarity 34.5%; Pred. No. 2.6e-17; Conservative 25; Mismatches 57; Indels 9
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-REB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
    ISLET NEOGENESIS
                                                            ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 LIWSSNECNKROHFLCKYR 157
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TELEPHONE: 202-508-9299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
'PMGTH: 174 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                            ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION: IS
UMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 48; Conserv
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CITY: Washington
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TOPOLOGY:
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  TITLE OF NUMBER OF
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86 YQRSQPIWIGLHDPQXRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CYYFWEDHLSWAEADLFCQNWNSG-YLVSVLSWAEGNFLASLIKESGTTAAN-VWIGLHD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 CYGYPRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.0%; Score 228.5; DB 2; Length 1
Best Local Similarity 34.5%; Pred. No. 2.6e-17;
Matches 48; Conservative 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID FITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID FILLOGULINS

IMMUNOSIDOBLINS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/185,670

FILLING DATE: 21-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 986,931

FILLING DATE: 16-DEC-1992

FILLING DATE: 16-DEC-1991

FILLING DATE: 16-DEC-1991

FILLING DATE: 16-DEC-1991

APPLICATION NUMBER: 808,122

FILLING DATE: 16-DEC-1991

APPLICATION NUMBER: 808,025
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.4%; Score 223; DB 6; 34.7%; Pred. No. 6.1e-17; tive 30; Mismatches 41
                                     FILING DATE: 09-SEP-1996
CLASSIFICATION: 435-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : |: |: |: |: | 155 LKWGDHHCDVELPFVCKFK 173
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                                                                                                                                                                                               32,141
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
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Search completed: December 31, 2003, 09:16:48
Job time : 43 secs
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                                                                                                                                             Sequence 2, Application US/08464637

Sequence 2, Application US/08464637

Patent No. 5834214

GENERAL INFORMATION:

APPLICANT: Iovanna, Juan-Lucio

APPLICANT: Bajorn, Jean-Charles

APPLICANT: Sarles, Josepher

APPLICANT: Sarles, Jean-Charles

APPLICANT: Sarles, Jean-Charles

APPLICANT: Sarles, Jean-Charles

APPLICANT: Sarlos

APPLICANT: Sarlos

APPLICANT: Sarlos

Dececion of Pancreatitis-Associated

TITLE OF INVENTION: Disease (as amended).

TITLE OF INVENTION: Disease (as amended).

TITLE OF INVENTION: Disease (as amended).

TITLE OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP

STREET: P.O. Box 747

CITY: Falls Church

COINNED VIEWED.

STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SG-NLVSVLSGAEGSFVSSLVKSIGNSYSYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLLSCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
99 PQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLFWSSNECNKRQHFLC 154
                             60 PKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKRWRDNSCDAQLSFVC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        • ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%; Score 221; 32.7%; Pred. No. 1
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Sequence 4, Application US/08401530A

Patent No. 5834590

GRNERAL INFORMATION:

APPLICANT: Vinik, Aaron I.

APPLICANT: Pittenger, Gary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MULPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,1977
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LILISCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
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Best Local Similarity 32.7%; Pred. No. 1.7e-16;
Matches 53; Conservative 29; Mismatches 64; Indels 16; Gaps
                                                  APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ISM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FLING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMULICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                   JUDRESS;
JUBERT: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: 100
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Rafaeloff, Ronit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-401-530A-4
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model Run on:

December 31, 2003, 09:22:09; Search time 2056 Seconds (without alignments) 1867.756 Million cell updates/sec US-09-525-041-2

878 1 MASRSMRLLLLLSCLAKTGV.....LIWSSNECNKRQHFLCKYRP 158 0.5 7.0 0.7 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

45562784 Total number of hits satisfying chosen parameters:

22781392 seqs, 12152238056 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

em_esthum:*
em_estin:*
em_estin:*
em_estin:*
em_estil:*
em_estil:*
em_htc:*
em_htc:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:* em_estba:* EST: *

em_gas_hum:* em_estfun:* 110::: 111::: 113::: 114::: 116::: 118::: 20:::

em_gss_fun:* em_gss_mam:* em_gss_mus:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_gss_pro:

em_gss_rod:* em_gss_phg:* em_gss_vrl:* gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	escription	5 K-EST004	72617 K-EST00	70898 60271910	4658 K-EST00	39168 K-EST000	31 K-EST	54067 K-ESTOLS	57953 EST37002	53845 60236654	38204 K-EST006	1779 EST186601	56113 602367	1222 nd38e09	1498 ni23g10	1286 ae62509.y	SAVID K-ESTOUD	1464 V-FCTC	1533 EST179353	990 EST1877	573 EST1864	1019 EST1788	789 EST1788	862 EST187607	BING K-ESTO	5/ ESTIB//	3549 EST1854	59144 K-ESTO	848 EST188510	92702 K-ESTO	3200 EST185134	BM796494 K-EST0079	M363214 CM3-C103	8128 CMD74	5249 EST18802	Y708034 BY708	08049 Mus mu	38108 ug48£05	08438 Mus musc	BM790284 K-EST00	513643 RZPD Mue	08339 BY7083	
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ALIGNMENTS

BM764955 663 bp mRNA linear EST 04-MAR-2002 K-EST0046563 S3SNU1681 Homo sapiens cDNA clone S3SNU1681-12-E07 5', mRNA sequence. BM764955 BM764955.1 GI:19094570 EST. RESULT 1 BM764955 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 663)

REFERENCE

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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                               Contact: Kim YS
Genome Research Center
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sz Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: E column: 07
High quality sequence stop: 663.
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Matches:
Conservative:
Mismatches:
Indels:
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cell type="Lymphoblast-like"

cell line="SNV-16"

llab_host="Topl0F""

clone_lib="S3SNU16s1"
                                                                                  21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="S3SNU1681-12-E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
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xref="taxon:9606"
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                                                                                                         Unpublished
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Best Local Similarity:
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JOURNAL
COMMENT
  AUTHORS
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8 8 8

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/clone libe 535NU1681"
/note= Torgan: Stomach; Vector: pT218RP1; Site_1: ECORI;
Site_2: Not1; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
with tabacch acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
i site by treatment of T4 RNA linkase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM772617 708 bp mRNA linear EST 04-MAR-2002
K-EST0056822 S3SNU1681 Homo sapiens CDNA clone S3SNU1681-14-G04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 708)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
207 CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT 266
                                                                                                                                                                                                                                                          81 GluTyr1leSerGlyTyrGlnArgSerGlnPro1leTrp11eGlyLeuHisAspProGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S1 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fax: +82-42-860-4409
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/cell_line="SNU-16"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 14 row: G column: 04
High quality sequence stop: 708.
Location/Qualifiers
1. 708
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S3SNU1661-14-G04"
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Homo sapiens
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BM772617
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Homo sapiens
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Query Match:
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priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toploř by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library. Atter analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blottinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA liberaries were constructed by transformation of the remaining DNA into competent cells E. coli Toplof' with
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mRNA sequence. BG770898

ACCESSION

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/organism="Homo sapiens"
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// db_zref="taxon:9607"
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// clone="Organ: prostate; Vector: pDNR-LIB (Clontech);
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// site_1: Sfi! (ggccgcccggcc); Site_2: Sfi (ggccattarggcc
// site_1: Sfi! (ggccgcccggcc); Site_2: Sfi (ggccattarggcc
// sapience: S'-ArTTARGCCGATTARGCCC-1; and 3' adaptor
// sequence: S'-ArTTARGCCGAGCGCGCC-1; and 3' adaptor
// sequence: S'-ArTTARGGCCGAGCGCGCC-1; and 3' adaptor
// sequence: S'-ArTTARGGCCGAGCGCGCGATTARGCC-1; and 3' adaptor
// sequence: S'-ArTTARGAGCCGAGGCGCGCATTARGCC-1; and 3' adaptor
// sequence: S'-ArTTARGCC-1; and 3' adaptor
// sequence: S'-ArTTARGAGCCGAGGCGCGAGGCGCG-1; and 3' adaptor
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                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTP/DTP

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCMA669 row: k column: 02

High quality sequence stop: 731.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone lib="Ascites lib poly (A)+ RNA was dephosphorylated with boatcerial alkaline phosphatase (TAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I slite by treatment of T4 RNA ligase and the first strand conA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The CDNA vector was adjusted to have about 6 Ont. The CDNA vector was adjusted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs where selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR
                                                                                                                                                                                                                                                                                                                                                               BM764658 665 bp mRNA linear EST 04-MAR-2002 K-EST0046207 S3SNU16s1 Homo sapiens cDNA clone S3SNU16s1-7-G11 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 665)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                         507
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                                            101 LygArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
388 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 447
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                                                                                                                                                                               508 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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21C Frontier Korean EST Project 2001
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/clone="S3SNU1681-7-G11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +82-42-660-4409
Email: yongsung@mail.kribb.re.kr
Plate: 7 row: G column: 11
High quality sequence stop: 665.
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JOURNAL
COMMENT
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AUTHORS
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products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells B. coli ToplOF' with electroporation method."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM739168 628 bp mRNA linear EST 01-MAR-2002
K-EST0008559 S3SNU16 Homo sapiens cDNA clone S3SNU16-3-G07 5', mRNA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 LeuGlyAspileileMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
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Mismatches:
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Best Local Similarity:
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BM739168
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1 (bases i Lo 600)

2 (bases i Lo 600)

2 (bases i Lo 600)

2 (bases i Lo 600)

3 (bases i Lo 600)

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9 (bases i Lo 600)

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5', mRNA sequence.
BM852931. GI:19209330
             121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
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                                                                                                                                                                           Contact: Kim YS
Contact: Kim YS
Genome Research Center
Genome Research Center
Genome Parent Institute of Bioscience & Biotechnology
Sz Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Exa: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 130 row: C column: 07
High quality sequence stop: 600.
Location/Qualifiers
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Conservative:
Mismatches:
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
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Pred. No.:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
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ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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BM852931
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/competent_cells E. coli Top10F' by electroporation method.
/clone_lib="S5SNU-16"
/clone
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Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470

Email: yongsung@mail.kribb.re.kr
Plate: 3 row: G column: 07

High quality sequence stop: 628.
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I. (Dasses 1 to 835)

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Onpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE872152 835 bp mRNA linear EST 20-OCT-2000 601446259F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850358 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                                                                                                                                                                                       351
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K-EST0136364 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-145-C05
BM854067
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Site_2: NotI, The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M. B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from
                                                                                                                                                                                                                                                                                                                                                     495
                                                                                                                                                                               GluTyrileSerGlyTyrGlnArgSerGlnProileTrpileGlyLeuHisAspProGln 100
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Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R. Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                       CTGGGTGATATCATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT
                                                                                                 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGGTATGGATTGGCCTGCACACAC
                                                                               CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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Plate: 145 row: C column: 05
High quality sequence stop: 667.
Location/Qualifiers
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BG253845 908 bp mRNA linear EST 13-FEB-2001 602366542F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4474691 5', mRNA sequence.
BG253845
BG253845.1 GI:12763661
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org
    Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
                                                                                                                                                                                                             1. .664
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5 a 160 c 173 g 156 t
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834.00
97.47$
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    ,I.E., Saeed,/
Quackenbush,J
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
#Worage insert size 1.8 kb. Library constructed by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 664)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
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218 c ;
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REFERENCE AUTHORS

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US-09-525-041-2 (1-158)
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                                                                                                                                                                               ACCESSION
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                 ò
                                                                                                                                                                                                                                                                                                                                                         l. 908
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/mol_type="maxNn"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Clones and constructed by Life Technologies.
Note: this is a NHH_MGC_Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysSerMetGlyGlydsnLysHisCysAlaGluMetSerSerAsnAsnRheLeuThr 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 908) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                             con Library Preparation: Life Technologies, Inc.
con Library Preparation: Life Technologies, Inc.
con Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10299 row: c column: 12
High quality sequence stop: 734.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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822.00
96.20%
96.20%
93.62%
Homo sapiens (human)
                   Homo sapiens
                                                                                                                          Unpublished
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/done liber=$358NU16"
//done liber=$1. Not: The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped inteat mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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K-EST0067322 S3SNU16 Homo sapiens CDNA clone S3SNU16-34-B05 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 580)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and YKim,Y.S.

21C Frontier Korean EST Project 2001
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
Esceun-dongongy, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Fax: +82-42-860-4409
Fax: +82-42-860-4409
Fight: 34 row: B column: 05
High quality sequence stop: 580.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
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BG256113 968 bp mRNA linear EST 13-FEB-2001 602367238F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4475648 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
              Email: arkerlav@tigr.org

Cor clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
Location/Qualifiers
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Matches:
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EST.
Homo gapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                           1.84e-79
785.00
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99.31$
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 Fax: 3018699423
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BG256113
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Best Local Similarity:
Query Match:
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VERSION
KEYWORDS
SOURCE
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BG256113
LOCUS
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I (bases 1 to 551)

Adams, M.D., Kerlavage, A.R., Fleischman, R.D., Fuldher, R.A., Bult

C.J., Lee, N.H., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White

(C.J., Lee, N.H., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White

(Jine, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M.,

Kalley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A., He, W.W.,

'Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Fueles, S.M., Dillion, P.J., Fannon

Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                 327 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCACCATAGCA 386
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                                                                                       TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGGTTCGAGTGTCAGTCT 326
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                                                                                                                                           9
                                                                                                                                                                                                                80
                    CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA314779.1 GI:1967108
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CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G. Consortium/LML at:
www-bio.llnl.gov/bbrp/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop; 410.
                                                                                                                                                           AA581222 440 bp mRNA linear EST 05-JAN-1998 nd38e09.rl NCI CGAP Col Homo sapiens cDNA clone IMAGE:802600 5' similar to SW:<u>IECG CROAT P21963 GALACTOSE-SPECIFIC LECTIN.</u>; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotki Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 440)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsnCysTyrGlyTyrPhe
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                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 968)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rollmingor. Rollmingor
High quality sequence stop: 672.
Location/Qualifiers
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/ Lissue_Lype="colon"

/ Lisb_host="DH10B"

/ Line_lib="NCI CGAP Co4"

/ Colo=_lib="NCI CGAP Co4"

/ Colo=_lib="NCI CGAP Co4"

/ Colo=="Vector: pry713D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled colon tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT713 vector. This library is not normalized. Library constructed by Bento Scares and M. Patima Bonaldo. "Inbrary constructed by Bento Scares and M. Patima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                           AI791498 13-DEC-1999 nRNA linear EST 13-DEC-1999 ni23g10.y5 NCI_CGAP_CO4 Homo sapiens cDNA clone IMAGE:968898 5' similar to SW.LECG_CROAT P21963 GALACTOSE-SPECIFIC LECTIN. ;, mRNA
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Oupublished
Other ESTs: ni23q10.s1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
                                         AsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThrTrpSerSerAsnGlu 145
TATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAGAAGAGGCAGCAGTGG 249
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
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This 5' resequenced clone has no previous 5' data to verify this
                                                                                                                                                                                                                      Insert Length: 1216 Std Brror: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 460.
Location/Qualifiers
1. .526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="hype="mRNA"
/db_xref="hype="mRNA"
/db_xref="hype="mRNA"
/db_xref="hype="mRNA"
/gex="pooled"
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                                                                                                                                                                                                                                                                                                      41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                                                                                                                                                                          61 TyrGlyAbnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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New isolated colon specific gene - used to develop prods. for use in the diagnosis and treatment of colon disorders, partic. colon
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· 编译 谷子
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Protein encoded by
Human colon specif
CS1-152 clone pred
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                                                                                                                                           December 31, 2003, 09:11:17; Search time 71 Seconds (without alignments) 353.223 Million cell updates/sec
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                  version 5.1.6
- 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                  GenCore (c) 1993
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Human colon cancer Amino acid sequence speci Human CENSET prote Human zinc finger Sequence encoded b Sequence encoded b Sequence encoded b MUREG-1. Mus musc Rat reg protein. Rat reg protein (G Rat reg pr
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95WO-US07169
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YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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         The present sequence represents a human Reg I-gamma protein, which comprises a C-type lectin. The sequence was identified in Incyte clone alloward Reg I-gamma protein is involved in regulation of cell growth and development. Since the overexpression of reg proteins is associated with tumourogenesis and neurodegeneration, inhibition of human Reg I-gamma expression can be used for treating or preventing neoplasia or metastasis and neurodegenerative changes associated with Alzheimer's disease and other disorders of the central nervous system, e.g. Down's syndrome. Reg I-gamma can also be used in therapeutics to induce products can also be used for detection for, e.g. expression of REG I-gamma, diagnosis and drug screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASRSWRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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100.0%; Pred. No. 1.3e-84;
tive 0; Mismatches 0;
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(SAGA ) SAGAMI CHEM RES CENTRE.
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                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Reg I-gamma protein; C-type lectin; Incyte clone 1310334; regulation; cell growth; development; tumourogenesis; neurodegeneration; inhibition; treatment; prevention, neoplasia; metastasis; neurodegenerative change; Alzheimer's disease; Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           A human colon specific protein (AAW12691) is a potential diagnostic marker for colon cancer. It is believed that the presence of active transcription of the colon specific gene in non-colon cells of a host is indicative of colon specific gene in non-colon cells sequence of the colon specific protein was deduced from a cDNA clone (AAT51784) isolated from a human colon cancer cDNA library. Recombinant colon specific protein can be produced in transformed host (e.g. bacterial, insect) cells and used to develop prods. for the diagnosis and treatment of colon disorders, partic. colon cancer metastasis. Antibodies raised against the protein can be used to target cancer cells and as part of a colon cancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human Reg I-gamma protein - useful for developing products for treating, e.g. diabetes, tumours or neuro-degenerative disease such as Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 878; DB 18;
illarity 100.0%; Pred. No. 1.3e-84;
Conservative 0; Mismatches 0;
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                                         Claim 1; Page 53; 64pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                      158 AA;
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cancer
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AAW37929

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Human protein comprising secretory signal amino acid sequence 3.
                                                                                               Human protein, secretory signal; nutritional source, cytokine; immunity; haematopoiesis; activin; inhibin; tumour; chemotactic; chemokinetic; thrombolytic; anti-inflammatory; inhibition;
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polypeptides.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is encoded by a human colon specific gene. The nucleic acid sequence can be used to develop products for the diagnosis of a disorder of the colon, e.g. colon cancer or metassases. The products can also be used to screen for agonists or antagonists for the polypeptides. The antagonists may be used to treat colon cancer, since they interact with the function of colon specific polypeptides to inhibit functions which are necessary for the viability of colon cancer cells. The products can also be used for the production of antibodies and for the identification of receptors for the
                                                                                                                                                                                                                                                                                                   1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                                                                                                                                                                                                                                                                 1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolysic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                 Length 158;
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                                                                                                                                                                                              ; Score 878; DB 19;
; Pred. No. 1.3e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by a human colon specific gene.
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                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 158; Conservative
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                                                                                                                                                           158 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a purified human protein, which is primarily expressed in tissue derived from the colon. The protein is 152 amino acids in length and exhibits cytoetatic activity. The present sequence represents the amino acid sequence of the colon specific protein. The protein can be used in the diagnosis and treatment of colon cancer, and it is thought that abnormally high levels of the gene expression in non-colon cells is an indication of colon cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human colon specific polypeptides and polynucleotides for diagnosis and treatment of colon cancer, for screening compounds which interact with polypeptide, for synthesis of DNA and manufacture of DNA
                                                                                                                                           1 MASRSMRILLILISCLAKTGVLGDIIMRPSCAPGWPYHKSNCYGYPRKLRNWSDAELECOS
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                                                                                                              1 MASRSMRLLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; colon specific; colon cancer; metastasis; diagnose; treatment;
                                                                                     Gaps
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                                                         Length 158;
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                                                                                                                                                                                                                                  KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP
                                                      ; Score 878; DB 20;
; Pred. No. 1.3e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon specific protein sequence.
                                                                                                                                                                                                                                                                                                                                     AAB12900 standard; Protein; 158
                                                        100.0%;
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                                                                    al Similarity 100.
158; Conservative
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                           158 AA;
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Matches
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                                                                      120
                                                                                                    61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes colon tumour associated proteins (I) and
YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
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                                                                                                                                                                                              121. KSMGGNRCHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                 121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CS1-152 clone predicted amino acid sequence.
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2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
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, Wang T,
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as diagnostic agents for detecting the presence of TCAPs in samples (e.g., by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI295 and AAM2494 to AAM24523 represent nucleoride and amino acid sequences given in the exemplification of the present invention.
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                                                                                                                                                                                                          100.0%; Score 878; DB 22; Length 158; 100.0%; Pred. No. 1.3e-84; ive 0; Mismatches 0; Indels 0
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15-FEB-2000; 2000US-0504629.
06-WAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
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Matches 158; Conservative
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                                                                                                                                                                                                                                         Local Similarity
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GE, Wang T,
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                                                                                                                                                                                                              Query Match
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activity of TCAPB by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (FCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity.

Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI2840 to AAI29512 and AAM2451 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
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19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
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15-FEB-2000; 2000US-0504629.
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Colon tumor associated proteins and nucleic acids useful for the

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The present invention describes colon tumour associated proteins (1) and the polynucleotides (11) that encode them. (1) have cytostatic activity. (1) and (11) can be used in gene therapy and vaccine production. (1) and (11) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) corpusation, and activity of cross associated with decreased expression by cativity of TCAPs by expressing inactive proteins or supplement the cativity of TCAPs by expressing inactive proteins or supplement the particles own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and the presence of similar nucleic acids in samples, and the presence of similar nucleic acids in samples, and the presence of similar nucleic acids in samples, and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate to the presence of similar nucleic acids in samples, and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to a diagnostic agents for detecting the presence of TCAPs in samples.

Chai:-(I) antibodies and antagonists may also be used to down regulate to a diagnostic agents for detecting the presence of TCAPs in samples.

Chai:-(I) antibodies and antagonists may also be used to down regulate and antagonists and antagonists may also be used to down regulate and antagonists and antagon
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prevention, diagnosis and treatment of colonic cancer
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
                                                                                        Claim 2; Page 467-468; 472pp; English.
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10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
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The present invention describes colon tumour associated proteins (1) and the polynucleotides (11) that encode them. (1) have cytostatic activity. (1) and (11) can be used in gene therapy and vaccine production. (1) and (11) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) carpression, such as colonic cancer. For example, (1) and (11) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the cativity of TCAPs by expressing inactive proteins or to supplement the produce the TCAPs by expressing inactive proteins or to supplement the produce the TCAPs by expressing inactive proteins or to supplement the production of them. Additionally, (11) may be used to call culturing the cell to express the protein. (11) and its call culturing the cell to express the protein. (11) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (FCR) and hybridisation assays to detect and the presence of similar nucleic acids in samples, and the assays to identify medulators of TCAP expression and activity. Anti-(1) antibodies and antagonists may also be used as antigens in the production of antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples. Anti-(1) antibodies and antagonists may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI29512 and AAMA4494 to AAMA4523 represent incleotide and aniho acid sequences and AAMA4494 to AAMA4523 represent incleotide and aniho acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                            Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                             Stolk JA;
                                                                                                                                                                Meagher MJ,
                                                                                                                                                          Benson DR,
                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 468; 472pp; English
                                                                                                                                                             Secrist H,
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
28-AUG-2000; 2000US-0649811.
                                                                                                                                                                                      King GE, Wang T, Jiang Y;
                                                                                                                                                                                                                                             WPI; 2001-441847/47.
                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                Lodes MJ,
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                                                                                                                                                          61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                             61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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                                                                              1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                        Gaps
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  Length 158;
                                        Indels
                                                                                                                                                                                                                                                         121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
100.0%; Score 878; DB 22;
100.0%; Pred. No. 1.3e-84;
tive 0; Mismatches 0;
                    Local Similarity 100.
    Query Match
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Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                               C880P similar amino acid sequence (GENESEQ W84274).
                       AAM24521 standard; Protein; 158 AA
                                                AAM24521;
RESULT 10
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                        Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer \,^{-}
                                                                                                                                                             Stolk JA;
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                                                                                                                                                              Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 878; DB 22;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 158; Conservative 0; Mismatches 0;
                                                                                                                                                              Benson DR,
                                                                                                                                                                                                                                    Claim 2; Page 469; 472pp; English
                                                                                                                                                              Secrist H,
                                                                                               06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
                                                                             10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629
                                                                                                                                                                      Jiang Y;
                                                   29-DEC-2000; 2000WO-US35596
                                                                                                                           28-AUG-2000; 2000US-0649811
                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                        WPI; 2001-441847/47.
                                                                                                                                                             Xu J, Lodes MJ,
King GE, Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA;
                WO200149716-A2
Homo sapiens.
                                  12-JUL-2001.
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YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for detecting REG-like protein (RELP) and its nucleic acid sequence. The method is useful for detecting the presence of a tumnur. Kits comprising an antibody specific for RELP and reagents for detecting the antibody, or a nucleic acid complementary to a portion of a nucleic acid encoding RELP, are useful for identifying the presence of cancer, characterise the cancer, or monitor the course of treatment of cancer. The present sequence is human RELP protein used to illustrate the method of the invention. Human RELP gene is located at
                                                                                                                                                                                                                                                                                                                                                                                  Detecting the presence of a tumor comprises detecting the concentration of a Reg Like Protein or the presence or quantity of a nucleic acid encoding it \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASRSWRLLLLLSCLAKTGVLGDIIMRPSCAPGWPYHKSNCYGYFRKLRNWSDAELECQS
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genetic analysis, diagnostic, antisense therapy.
                                                       23..158
/note= "Human mature REG-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                     (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
1..22
/label= Signal_peptide
23..158
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 13-14; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB78993 standard; Protein; 158 AA
                                                                                                                                                                                15-MAR-2002; 2002EP-0251876
                                                                                                                                                                                                                    16-MAR-2001; 2001US-276414P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                               WPI; 2002-684095/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA;
                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD47239
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                                                                                                          EP1241269-A2
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                                                                                                                                                                                                                                                                                           Heiskala M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                       Protein
                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has panceatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; REG-like protein; RELP; tumour; cancer; therapy; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding a polypeptide useful for the diagnosis and
                                                                                                                                                                              Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSA7005 gene, encoding a polypeptide useful for the distreatment of diseases associated with its expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
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                                                                                                                                            Human TSA7005 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 23; 25pp; Japanese.
                                AAB74934 standard; Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE29829 standard; Protein; 158
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                                                                                                                                                                                                                                                                                                                                              99JP-0201279
                                                                                                                                                                                                                                                                                                                                                                                  99JP-0201279
                                                                                                                                                                                                                                                                                                                                                                                                                    (SAKA ) OTSUKA PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-303742/32.
N-PSDB; AAF82117, AAF82118.
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                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 AA;
                                                                                                                                                                                                                                                                    JP2001025389-A.
                                                                                                        27-JUN-2001
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999;
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                                                                                                                                                                                                   diagnosis.
                                                                  AAB74934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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RESULT 12

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Key

#X8X#XBX#X8X#

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Length 158; Indels

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The present sequence represents a new isolated REG-like protein (RELP) human immunoglobulin (Ig) derived protein. RELP comprises: (a) a human variable and connetant region, or (b) an isolated human Ig derived protein or specified portion or variant encoded by a nucleic acid. RELP has cytostatic activity and can be used as an Ig agonist and in protein threrapy. The RELP human Ig derived protein or a specified portion or variant can be used for preventing or treating a RELP protein mediated condition, malignant condition or disease condition, e.g. cancer. The nucleic acids can be used in producing RELP Ig derived chromosome 1p12-13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated REG-like protein (RELP) human immunoglobulin derived protein or specified portion or variant, useful for preventing or treating a RELP protein mediated condition or malignant condition, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 101pp; English.
/label= signal
                          27..158
/label= RELP
                                                                                                                                                                                                14-MAR-2002; 2002WO-US07945
                                                                                                                                                                                                                                                  16-MAR-2001; 2001US-276305P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                   (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-103204/09.
N-PSDB; ABZ21635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA;
                                                                                                   WO200274916-A2
                                                                                                                                                 26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                     Heiskala M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78991 to ABB79004 represent proteins encoded by the ABQ60775 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide cuced by (I) is useful for detecting cancer in a patient sample, and cor detecting the presence or absence of a polynuclectide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a pyridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysie, mapping and diagnostic applications. (I) can be used to raise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                                                                                                                                                                         Catino TJ, Dwivedi P, Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analysis, mapping and diagnostic applications. (I) can be used tantibodies, and to screen for peptide analogues and antagonists.
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Pred. No. 1.3e-84;
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                                                                                                                                                                         Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 3; 796pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                          02-OCT-2001; 2001WO-US30732.
                                                                        02-OCT-2000; 2000US-237271P.
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Matches 158; Conservative
                                                                                                                                                                         Burgess C, Astle JH, Ca
Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                  WPI; 2002-426115/45.
N-PSDB; ABQ60776.
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Best Local Similarity
                                                                                                                       (FARB ) BAYER CORP.
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                    9
                                                                                                                                                                   61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                      1 MASRSMRILLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer; tumour; immune response; immunostimulant; cytostatic; vaccine.
                                          ö
100.0%; Score 878; DB 24; Length 158; 100.0%; Pred. No. 1.3e-84; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon tumour protein for clone CS1-152 SEQ ID NO:1070.
                                                                                                                                                                                                                                                                     121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                              ABP55366 standard; Protein; 158 AA.
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Location/Qualifiers

Homo sapiens

RESULT 14

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셤 ò Peptide

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XX XX XV 10-APR-2001; 2001WS-0831263.
PR 10-APR-2001; 2001WS-0831263.
PR 10-APR-2001; 2001WS-0831263.
PR 10-APR-2001; 2001WS-0921217.
PR 19-DEC-2001; 2001WS-0921317.
PR 19-DEC-2001; 2001WS-0921317.
PR 19-DEC-2001; 2001WS-0921317.
PR 19-DEC-2001; 2001WS-0921300.
XX (CORI-) CORIXA CORP.
XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
PI Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD;
PI Skeiky YAW, Fanger GR, Vedvick TS, Carter D;
PI Skeiky YAW, Fanger GR, Vedvick TS, Carter D;
PR WHP; 2003-067548/06.
DR WP5DB; AB233691.
XX YX YX WPT; 2003-067548/06.
DR WP5DB; AB233691.
XX PT New polymucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer - TX Disclosure; Page 465; 537pp; English.
XX The present invention describes compounds (I) for the immunotherapy and CC diagnosis of colon cancer. Also described: (I) a method for stimulating and immune response in a patient; (3) an isolated T cell specific for a tumour protebi; (3) an isolated T cell comprising T cells prepared by the method of (2); (4) a method CC expanding T cells specific for a tumour protebi; (3) an isolated T cell comprising T cells prepared by the method of (2); (4) a method CC expanding an immune response in a patient; (6) a method for inhibiting the Corporation comprising an immune response in a patient; (6) a method for inhibiting the Corporation and Can be used in vaccines. AB232646 to AB23325 CC and ABP55331 tepresent human colon cancer/tumour related Sequence 158 AA;
Sequence 158 AA;
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 Query Match
 100.0%;
 Score 878;
 DB 24;
 Length 158;

 Best Local Similarity 100.0%;
 Pred. No. 1.3e-84;
 Gaps
 O
 Indels 0;
 Gaps
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 QY
 IMASRSMRLLLLISCLAKTGVLGDINMPPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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 QY
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 61 YGNGAHLASILSLKBASTIABYISGYRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
 120

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 61 YGNGAHLASILSLKBASTIABYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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Search completed: December 31, 2003, 09:13:34 Job time : 72 secs

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- L3 ANSWER 58 OF 59 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 4
- AN 1993:432762 BIOSIS
- DN PREV199396087387
- TI A gene homologous to the reg gene is expressed in the human pancreas.
- AU Bartoli, Catherine; Gharib, Bouchra; Giorgi, Dominique; Sansonetti, Alice; Dagorn, Jean-Charles; Berge-Lefranc, Jean-Louis [Reprint author]
- CS Unite 315 l'INSERM, 46 Boulevard Gaye, 13258 Marseille Cedex 9, France
- SO FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol. 327, No. 3, pp. 289-293.

 CODEN: FEBLAL. ISSN: 0014-5793.
- DT Article
- LA English
- OS Genbank-L08010
- ED Entered STN: 22 Sep 1993 Last Updated on STN: 6 Nov 1993
- AB We have determined the nucleotide sequence of reg1 a human genomic DNA fragment homologous to the reg gene which is expressed in the exocrine pancreas and regenerating islets. Sequence comparisons of reg and reg1 suggested similar exon-intron organisation. Based on this assumption, specific oligonucleotides for reg1 exons were used to demonstrate expression of the reg1 gene in pancreas and liver, The proteins encoded by reg and reg1 comprise 166 amino acids and differ by 22 amino acids only.

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: . December 31, 2003, 09:11:17 , Search time 38 Seconds
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Run on: December 31, 2003, 09:11:17; Search time 38 Seconds (without alignments)
195.532 Million cell updates/sec Title: US-09-525-041-2
Perfect score: 878
Sequence: 1 MASRSWRLLLLESCLAKTGV......LTWSSNECNKRQHFLCKYRP 158

Sequence: 1 MASRSMRLLLLLSCLAKTGV...
Scoring table: BLOSUN62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		d			SUMMARIES	
Result No.	Score	Query	Length	BO	ΙD	Description
-	258.5	29.4	132	: -	ACAL ANSAN	P83300 anser anser
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10	231		175	-	LITH BOVIN	
11	228.5		174	Н	PAP2_RAT	P35231 rattus norv
12	225.5		166	-	LITA_HUMAN	
13	222.5	25.3	172	-	LECA PLEWA	Q02988 pleurodeles
14	221		175	-1	PAP1 HUMAN	
15	218.5		158	-	LECG_TRIST	trime
16	203	23.	175	Н	PAP1 RAT	
17	202.5	33.	123	-	ECHB_ECHCA	
18	202.5	23.	152	Н	IXA_TRIFL	P23806 trimeresuru
19	199.5	55	134	н	ABA2 TRIAB	
20	197.5	22.5	125	н	ABA3 TRIAB	P81113 trimeresuru
21	196.5	22.	146	-	IXB TRIFL	-
22	194	22.1	175	Н	PAP1 MOUSE	P35230 mus musculu
23	193	22.	912	Н	PGCB BOVIN	Q28062 bos taurus
24	191	21.	883	Н	PGCB_MOUSE	Q61361 mus musculu
25	190	27	175	Н	PBCG HUMAN	Q92778 homo sapien
56	189	21.5	133	н	BOTA_BOTJA	
27	186.5	1.	131	н	ABA1 TRIAB	
28	186.5	21.2	132		ABBA_TRIAB	P81115 trimeresuru
29	185.5	\sim	125	ч	BOTB_BOTJA	P22030 bothrops ja
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P07306 homo sapien Q90953 gallus gall P55066 mus musculu Q9erb4 rattus norv G62059 mus musculu P13611 homo sapien P07307 homo sapien P07439 megabalanus P07439 crotalus du P81282 bos taurus O99426 crotalus du P81509 crotalus du
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ALIGNMENTS

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ACAL ANSAN ACAL ANSAN ACAL ANSAN B1330 A. B1300 A. STANDARD; PRT; 132 AA. B8 FEB-2003 (Rel. 41, Created) 28 FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Ansocalcin. Anser anser anser (Western graylag goose). Ekkaryota, Metazoa; Chordata; Craniata; Vertebrata; Bute; BLARTOCALS, Metazoa; Chordata; Craniata; Vertebrata; Bute; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; A. NCBI TaxID=8844; [1] SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, AND M. SPECTROMETRY. TISSUE=Bggshell matrix; Medbed=12431998; Lakehminarayanan R., Valiyaveettil S., Rao V.S., Kini R., "Purification, characterization, and in vitro mineralizat of a novel goose eggshell matrix protein, ansocalcin; J. Biol. Chem. 278-298-2936(2003) -!- FUNCTION: Induces spherical aggregates of calcite cry vitro. Believed to play an active role in the eggshell -!- SUBUNIT: Homodimer or homotrimer. -!- SUBUNIT: AND NESSER BESTANDER AND NESSER AN	glands on the Walls of Oviduct and incorporated into the granted control of the Walls of Oviduct and incorporated into the granted control of the Saminaria is a Saminaria in C-type lectin family domain. -!- SIMILARITY: Contains 1 C-type lectin family domain. InterPro: IPR001391; AntifreeZeII. InterPro: IPR001304; Lectin C. PRINTS: PR00159; PROTEATITSAP. PRINTS; PR00159; PROTEATITSAP. PRINTS; PR001504; PROTEATITSAP. PROSITE; SW00034; CLECT; 1. PROSITE; PS00615; C_TYPE_LECTIN 1; 1. PROSITE; PS0061; C_TYPE_LECTIN 2; 1.		Query Match 29.4%; Score 258.5; DB 1; Length 132; Best Local Similarity 34.3%; Pred. No. 4.5e-19; Matches 46; Conservative 25; Mismatches 50; Indels 13; Gaps	SO CAFORETANNICTOFF FALLEN WEDGELCOUNTING THE STANDARD TO STANDARD	90 QPIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNKHCAEMSSNNNFLTWS
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::||||| ::|::| EEEDNVWIGLH-----HWNQARVWIDGSKKRYSAWDDDELPRGKYCTVLEGSSGFMSWE 116
                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update)
Lichostathine 1 precursor (Pancreatic stone protein 1) (PSP)
(Pancreatic thread protein 1) (PTP) (Islet of langerhans regenerating protein 1) (REG 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: EXPRESSED ONLY IN RECENERATING ISLETS AND NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS. EXPRESSED STRONGLY IN PANCREAS, MODERATELY IN GALLBLADDER, AND WEAKLY IN LIVER.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H., Moriizumi S., Okamoto H., Itoh T., Teraoka H.;
"Structure, chromosomal localization, and expression of mouse reg genes, reg I and reg II. A novel type of reg gene, reg II, exists
                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the mouse genome.";
J. Biol. Chem. 268:15974-15982(1993).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CARBONATE PRECIPITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
LITHOSTATHINE 1.
C-TYPE LECTIN (LONG FORM).
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                                                                                                                                                                165 AA.
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PROSITE, PS50041, C_TYPE_LECTIN_2; 1.
                                                                                                                                                                PRT;
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InterPro, IPR001304; Lectin C.
InterPro, IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J;
MEDLINE-93340209; PubMed-8340418;
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PRINTS; PR01504; PNCREATITSAP.
PRINTS; PR00356; ANTIFREEZEII.
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                                                 143 SNECNKRQHFLCKY 156
                                                                   | |::| |:||
117 DNACSERNPFVCKY 130
                                                                                                                                                                STANDARD;
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MGD; MGI:97895; Reg1
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                                                                                                                                                              LIT1 MOUSE
P43137;
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                                                                                                                                               MOUSE
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29.0%; Score 254.5; DB 1; Length 165;

Query Match

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7.
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                                                                                                                                                       55 ELECQSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWIDGAM 112
                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Lithostathine precursor (Pancreatic atome protein) (PSP) (Pancreatic thread protein) (PTP) (Islet of langerhans regenerating protein) (REG) (Islet cells regeneration factor) (ICRF).
                                                                                                               8 ILLSCL-----IVLSPSQGQEAEEDLPSARISCPEGSNAYSSYCYYFTEDRLTWADA
                                                                         ---SCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovery M.;
Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovery M.;
"Characterization in rat pancreatic juice of a protein homologous to
the human pancreatic stone protein ";
comp. Biochem. Physiol. 318:793-797 (1989).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CARBONATE PRECIPITATION.
-!- TISSUE SPECIFICATY: EXPRESSED ONLY IN REGENERATING ISLETS, BUT
NOT IN NORWAL PANCREATIC ISLETS, INSULINOMAS OR REGENERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDIATE=1903273; PubMed=1985964;
MEDIATE=1903273; PubMed=1985964;
Rouguier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.;
"Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine cells, regulation by food content, and sequence identity with the endocrine reg transcript.";
J. Biol. Chem. 266:786-791(1991).
                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88115343; PubMed=2963000;
Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y., Tochino Y., Okamoto H.;
Tochino Y., Okamoto H.;
The novel gene activated in regenerating islets.";
J. Brovel gene 263:2111-2114(1988).
                                                                                                                                                                                                                                       113 YLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                                                                              118 FLYKSWATGSPNSSNRGYCVSLTSNTGYKKWKDDNCDAQYSFVCKFY 164
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:
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyashita H., Suzuki Y., Watanabe T., Unno M., Moriizumi Yonekura H., Okamoto H., "Structure and characterization of rat Reg I gene."; Selkagaku 65:1082-1082(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vanna J.L.;
of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dusetti N.J., Frigerio J.M., Dagorn J.-C., Iovanna "Rapid PCR cloning and sequence determination of the
              Pred. No. 1.4e-18;
5; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1174:99-102(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93326645; PubMed=7916640;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                           10 LLLSCLAKTGVLGDIIMRP-
                                   52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lithostathine genē."
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pancreas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REG1 OR REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIVER.
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PAP2 OR REG3A.
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                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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009037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAP2_MOUSE
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its enter is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYFILLSCL------MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 RLLLLLSCLAKTGVLGDIIMRPS------CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure, chromosomal localization and expression of mouse genee
encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNBCNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWNRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                                                                                              . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Score 254.5; DB 1; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 3 precursor (REG III-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Indels
 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                               18672 MW; 9B61EB236B82CF8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas; MEDLINE=97208868; PubMed=9055810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 AA
                                                                                                                                                                                                                                                                                                                                 LITHOSTATHINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Mismatches
                                                                                                                                                                                                                                                                         PROSITE; PS00615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C TYPE LECTIN 2; 1. Glycoprotein; Signal; Lectin.
                                                                                                                                                                                                          Interpro; IPR001304; Lectin C.
Interpro; IPR003990; Pancreatis ac.
Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                EMBL; L07512; AAA41533.1; -.
EMBL; M62930; AAA41974.1; -.
                                                                                                                                          EMBL; M62930; AAA41974.1; -
EMBL; M18962; AAA42028.1; -
EMBL; D26164; BAA05149.1; -
PIR; A28351; A28351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
                                                                                                                                                                                                                                                                 SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP3 OR REG3G.
                                                                                                                                                                                                P05451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAP3 MOUSE
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                                                                                                                                                                                                                                                                                                                                                         DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 NGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDP-----QKRQQWQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG-HLVSVLSGAEASFLSSMIKSSGNSGQYVWIGLHDPTLGYEPNRGGWEWSNADVMNYI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LLLSCL-AKTGVLGDII-----MRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 MILISCLMILISOVOGEVAKKDAPSSRSSCPKGSRAYGSYCYALFSVSKWWYDADMACOKRP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTE; PS00615; C.TYPE LECTIN 1; FALSE NEG.
PROSTE; PS00615; C.TYPE LECTIN 2; 1.
Signal; Lectin; InflammaTory response; Acute phase; Multigene family.
Signal 1 26
POTENTIAL.
CHAIN 27 174
PANCREATITIS-ASSOCIATED PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet of langerhans regenerating protein 3) (REG 3) (REG III-alpha).
                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL BACTERIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;
MEDLINE=97208868; Pubmed=9055810;
Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEALTHY PANCREAS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5575E9E56A4D8CEF CRC64;
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.1%; Score 246.5;
35.2%; Pred. No. 9.8e
iive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; PO5451; 1LIT.
MGD; MGI:109406; Reg3g.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D63361; BAA18930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D63362; BAA18931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 35.2 tes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
170
162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 1
174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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us-09-525-041-2.rsp

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                Moriizumi S., Watanabe T., Unno M., Nakagawara K.I., Suzuki Y., Miyashita H., Yonekura H., Okamoto H., "Isolation, structural determination and expression of a novel reggene, human regI beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   "The glycan moiety of human pancreatic lithostathine. Structure characterization and possible pathophysiological implications.";

Eur. J. Balochem. 230:503-510(1995).

-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.

-!- PTW: ALL O-LINKED GLYCANS CONSIST OF GAL-GLCNAC-GAL-GALNAC TETRASACCHARIDS CORE AND GET ELONGATED (MICROHETEROGENEITY).

-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LITHOSTATHINE 1 BETA.
C-TYPE LECTIN (LONG FORM).
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
O-LINKED (GALNAC. . ) (MUCIN TYPE).
BY SIMILARITY.
                                                                                                                                                                                  MEDLINE-93351647; PubMed-8348956;
Bartoli C., Gharib B., Giorgi D., Sansonetti A., Dagorn J.-C.,
Berge-Lefranc U.;
                                                                                                                                                                                                                                                                                                                                                                                            De Reggi M., Capon C., Gharib B., Wieruszeski J.M., Michel R.,
                                                                                                                                                                                                                                                        'A gene homologous to the reg gene is expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00059; lectin c; 1.

SMARY: SROUSH, CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Glycoprotein; Signal; Lectin Pyrrolidone carboxylic acid.
SIGNAL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 167771; -.
GO; GO:0008283; P:cell proliferation; TAS.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                              3iochim. Biophys. Acta 1217:199-202(1994).
                                                                                                                                                                                                                                                                                                                                                 CARBOHYDRATE-LINKAGE SITE.
MEDLINE=95331286; PubMed=7607222;
MEDLINE=94153997; PubMed=8110835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D17291; BAA04124.1; -.
EMBL; D16616; BAA04091.1; -.
EMBL; L08010; AAA18204.1; -.
PIR; S34501; RGHU1B.
HSSP; P05451; 1LIT.
Genew; HGNC:9952; REGIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 BY
18665 MW;
                                                                                                                                                                                                                                                                                                   FEBS Lett. 327:289-293(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
166 AA;
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 NGAHLASILSLKEASTIAEYISG-YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LLLSCLAKT-GVLGDIIM-----RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal, Lectin, Inflammatory response, Acute phase, Multigene family.
Signal, Lectin, Inflammatory response, Acute phase, Multigene family.
Signal 1 26 BY SIMILARITY.
DOMAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 2.
DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
DISULFID 40 51 BY SIMILARITY.
DISULFID 68 171 BY SIMILARITY.
DISULFID 146 163 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Gaps
                        "Structure, chromosomal localization and expression of mouse genes
                                                                                         FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF BACTERIAL PROLIFERATION.
                                                                                                                                    -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: SMALL INTESTINE, AND PANCREAS.
-:- DISEASE: OVEREXERSESED DURING THE ACUTE PHASE OF PANCREATITIS.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
                                      encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lithostathine 1 beta precursor (Regenerating protein I beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.6%; Score 242; DB 1; Length 175; 34.4%; Pred. No. 2.8e-17; ive 27; Mismatches 64; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 SWSG--KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3E311B3976E80F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (60 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE_LECTIN_1; 1.
_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:109408; Reg3a.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00059, lectin c; 1.
PRINTS, PR01504, PNCREATITSAP.
SMART, SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 AA; 19539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, D63356; BAA18925.1; -.
EMBL, D63357; BAA18926.1; -.
EMBL; D63358; BAA18927.1; -.
HSSP; P05451; 1LIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00615; C
PROSITE; PS50041; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGIB OR REGL
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P48304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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87 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSS 143
                                                                                                                                                              27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGY
                                                                                                                                                                                      33 RISCPEGTNAYRSYCYYFNEDPETWVDADLYCQNMNSG-NLVSVLTQAEGAFVASLIKES
                                                                                                                        4.
                                                                              Length 166;
                                                                                                                    57; Indels
                                          DIDC20E11AE5DDE8 CRC64;
                                                                              27.3%; Score 240; DB 1; 34.3%; Pred. No. 4.2e-17;
                                                                                                                      27; Mismatches
SIMILARITY
                   SIMILARITY
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SEQUENCE FROM N.A NCBI_TaxID=9606;

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TISSUE=Pancreas;

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Gaps

105 118

9 47

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89 SQP-IWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASRSMRLLLLLSCLAKTGVLGDII-------MRPSCAPGWFYHKSNCYGYFRK
                                                                 48 LRNWSDAELECOSYGNGAHLASILSLKEASTIAEYI -- SGYORSOPIWIGLHDPOKROOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91115849; PubMed=1989986; Hirabayashi J., Kusunoki T., Kasai K.-I.; Harabayashi J., Kusunoki T., Kasai K.-I.; "Complete primary structure of a galactose-specific lectin from the venom of the rattlesnake Crotalus atrox. Homologies with Ca2(+)-
                                                                                                                                                                                                 106 QWIDGAMYLYRSWS--GKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                         119 HWSSGSLFLFKSWATGAPSTANRGYCVSLTSNTAYKKWDENCEAQYSFVCKFR 172
                                                                                                                                                                                                                                                                                                                                                                                                                          Galactose-specific lectin.
Crotalus atrox (Western diamondback rattlesnake).
Crotalus atrox (Western diamondback rattlesnake).
Evolutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 135
  72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: Contains 1 C-type lectin family domain. PIR; A38609; A38609. HSSP; P22897; LEGG. InterPro; IPR001353; Antifreezell. InterPro; IPR001304; Lectin.C. InterPro; IPR001304; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16291 MW; 04BAC45DB2B721C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.5%; Score 233; DB 1; 34.4%; Pred. No. 1.7e-16; ive 18; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          135 AA
    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00059, lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE LE
PROSITE; PS50041; C_TYPE_LE
Calcium; Lectin. 135
    50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Conservative
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                      LECG CROAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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CROAT
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Matches
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STDDSNVWIGLHDPKKARRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lithostathine 2 precursor (Pancreatic stone protein 2) (PSP)
(Pancreatic thread protein 2) (FTP) (Islet of langerhans regenerating protein 2) (REG 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS. EXPRESSED STRONGLY IN PANCREAS, WEAKLY IN LIVER, BUT NOT AT ALL IN GALLBLANDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93340209; PubMed-8340418;
Unno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H.,
Moriizumi S., Okamoto H., Itoh T., Teraoka H.;
"Structure, chromosomal localization, and expression of mouse reg
genes, reg I and reg II. A novel type of reg gene, reg II, exists
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 268:15974-15982 (1993).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 236.5; DB 1; Length 173; Pred. No. 9.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LITHOSTATHINE 2.
C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7D34C4DAB232F25C CRC64;
                                                                                                                                                                                                   173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:97896; Reg2.
InterPro; IRR00233; Antifreezell.
InterPro; IRR003104; Lectin_C.
InterPro; IRR00390; Pancreatis_ac.
Pfam; PP00059; lectin_c; l.
RRINTS; PR01504; PNCREATITSAP.
PRINTS; SR00516; ANTIFREEZELI.
SMART: SM00014; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTIN_1; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D14011; BAA03112.1; -. PIR; B47148; B47148.
HSSP; P05451; 1LIT.
                                                           144 NECNKRQHFLCKYR 157
                                                                                    | |: |:||::
152 ESCEKKFSFVCKFK 165
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the mouse genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Lectin.
SIGNAL
                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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61

Query Match

DOMAIN CHAIN

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LITH BOVIN P23132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                  LITH_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
62 GQENVWIGLRDKKKDFSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLMNDQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VALTTMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA 64
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Intestine;
MEDLINE=Sprague-Dawley; TISSUE=Intestine;
MEDLINE=94060113; PubMed=8241280;
Frigerio J.-M., Dusetti N.J., Garrido P., Dagorn J.C., Iovanna J.L.;
Frigerio J.-M., Dusetti N.J., Garrido P., Dagorn J.C., Iovanna J.L.;
The pancreatitis associated protein III (PAP III), a new member of
the PAP gene family.";
Biochim. Biochim. Bach Acta 1216:329-331(1993).
-!- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
BACTERIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PANCREATITIS-ASSOCIATED PROTEIN 3.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.3%; Score 231; DB 1; Length 174; 32.4%; Pred. No. 3.5e-16; ive 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5CED2E887C46E45C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Lectin; Inflammatory response; Acute phase. SIGNAL 1 26 POTENTIAL.
                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-RDS-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                   174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S54979; S54979.
HSSP; P05451; 1LIT.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19143 MW;
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                                                                ECNKRQHFLCK 155
                                                                                                        122 VČESKDAFLČO 132
                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
38
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68
145
174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                145
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                                                                                                                                                                                                                                   P42854;
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                                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islat of langerhans regenerating protein) (REG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90368981; PubMed=2394826;
de la Monte S.M., Ozturk M., Wands J.R.;
"Enhanced expression of an exocrine pancreatic protein in Alzheimer's
disease and the developing human brain.";
J. Clin. Invest. 86:1004-1013(1990).
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N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82298214; PubMed=3862086; Gross J., Brauer A.W., Bringhurst R.F., Corbett C., Margolies M. Gross J., Brauer A.W., Bringhurst R.F., Corbett C., Margolies M. "An unusual bovine pancreatic protein exhibiting pH-dependent globule-fibril transformation and unique amino acid sequence."; Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631 (1985).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: CLEAVED TO GIVE AN A CHAIN AND A B CHAIN JOINED BY
109 DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                            124 NADVMNYFNWETNPSSVSGSHCGTLTRASGFLRWRENNCISELPYVCKFK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 38-138 AND 141-175.
BEDILINE-3197388; Pubmed=208387;
Cai L., Harris W.R., Marshak D.R., Gross J.; Crabb J.W.;
"Structural analysis of boyine pancreatic thread protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS.
                                                                                                                                                                                                                                          175 AA
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LITHOSTATHINE.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Glycoprotein; Signal; Lectin.
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InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Protein Chem. 9:623-632(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M59794; AAA30750.1; -.
                                                                                                                                                                                                                                          STANDARD;
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37
175
138
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LITA HUMAN
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               DOR NO DO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 SYGNGAHLASILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQ-----WQWIDGAMY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 KRPSG-HLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSEANAGGWEWISNDVL 128
                                                                                                                                                                                                                                                                                                                                                                                                             23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLSCLAKTGVLGDI-----IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE=93378971; PubMed=8369291;
Frigerio J.-M., Dusetti N.J., Keim V., Dagorn J.C., Iovanna J.L.;
Identification of a second rat pancreatitis-associated protein.
Messenger RNA cloning, gene structure, and expression during acute pancreatitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- SINCELLULAR LOCATION: Secreted.
-!- INDUCTION SPEARS IN PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC INFLAMATION.
-!- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                          26.3%; Score 231; DB·1; Length 175; llarity 30.9%; Pred. No. 3.5e-16; Conservative 30; Mismatches 62; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 NYVAWETDPAAISSPGYCGSLSRSSGYLKWRDHNCNLNLPYVCKF 173
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           C-TYPE LECTIN (LONG FORM).
                                                                                                                                                   E -> FF (IN REF. 3).
C270EE70B7E91D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
of langerhans regenerating protein 3) (REG 3).
PAP2 OR REG3.
                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
EE -> FF (IN REI
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MEDLINE-94314238; PubMed-8039722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 32:9236-9241 (1993).
173 C-
51 BY
171 BY
163 BY
85 EE
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   38 1
40
68 1
146 1
175 AA;
                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                 51,
   DOMAIN
DISULFID
DISULFID
DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                             Query Match
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86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LITA HUMAN STANDARD; PRT; 166 AA.
P05451; P11379;
01-NOV-1988 (Rel. 09, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Lithostathine 1 alpha precursor (Pancreatic stone protein) (PSP)
(Pancreatic thread protein) (PTP) (Islat of langerhans regenerating protein) (REG) (Regenerating protein I alpha) (Islat cells regeneration factor) (ICRP).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                       PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88115343; PubMed-2963000;
Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y., Tochino Y., Okamoto H.;
Takasawa S., Shiga K., Yonemura Y.,
Tachino Y., Okamoto H.;
Takasawa S., Shiga K., Yonemura Y.,
J. Biol. Chem. 263:2111-2114(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                                                     C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
W -> G (IN REF. 2).
A; 4530B884496E5888 CRC64;
                                                                                                                                                                                                 PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Signal; Lectin; Inflammatory regponse; Acute phase..
SIGNAL 1 25
PW SIMILARITY.
CHAIN 26 174
PANCREATITIS-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%; Score 228.5; DB 1
34.5%; Pred. No. 6.3e-16;
tive 25; Mismatches 57
                                                  PIR, A48689; A48689.
PIR, 160296; 183377.
HSSP, P05451; 11.17.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
PEm; PF00059; Lectin_C; 1.
PRINTS; PR01504; PNCREATITSAP.
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J. Biol.,Chem. 265:7432-7439(1990)
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MEDLINE=90237042; PubMed=2332435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                      19599 MW;
                  D26078; BAA05071.1;
D23676; BAA04904.1;
EMBL; L10229; AAA02980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                       SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                   174
172
172
170
162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                               DISULFID
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Best Local
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                  EMBL;
EMBL;
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MEDLINE=22388257; PubMed=12477932;
Straubberg R.L. Feingold E.A. Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan.H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan.H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M.J., Usdin T.B., Proshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gross J., Carlson R.I., Brauer A.W., Margolies M.N., Warshaw A.L., Wands J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=89150292; PubMed=2493268; de Caro A.W., Adrich Z., Fournet B., Capon C., Bonicel J.J., de Caro J.D., Rovery M. "Netrich Z., Fournet B., Capon C., Bonicel J.J., Movery M. "N-terminal sequence extension in the glycosylated forms of human pancreatic stone protein. The 5-oxoproline N-terminal chain is Oglycosylated on the 5th amino acid residue."; biophys. Acra 994:281-284(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-166.
MEDLINE-88029417; PubMed-3665916;
de Caro A.M., Bonicel J.J., Rouimi P., de Caro J.D., Sarles H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Partial amino acid sequence of human pancreatic stone protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wontalto G., Bonicel J.J., Multigner L., Rovery M., Sarles H.,
                                                                                                                                                                  "Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and expression in chronic calcifying pancreatitis."; J. Clin. Invest. 84:100-106(1989).
                                                                                                 Giorgi D., Bernard J.-P., Rouquier S., Iovanna J., Sarles H.,
Dagorn J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation, characterization, and distribution of an unusual pancreatic human secretory protein.", J. Clin. Invest. 76:2115-2125(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete amino acid sequence of an immunoreactive form of pancreatic stone protein isolated from pancreatic juice."; Eur. J. Biochem. 168:201-207(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                Boonyasrisawat W., Tandhanand-Banchuin N., Vannasaeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Biochem. J. 238:227-232(1986),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87099950; PubMed=3541906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86086356; PubMed=3908481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 33-58.
MEDLINE=87219142; PubMed=3108036;
                                                                        MEDLINE=89292148; PubMed=2525567;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 23-47.
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                                                                                                                                                                                                                                                                                                                                                                                                           ALZHEIMER'S DISEASE AND DEVELOPMENTAL EXPRESSION REGULATION.
MEDILINE=90368981; PubMed=2294826;
de la Monte S.M., Ozturk M., Wanda J.R.;
"Enhanced expression of an exocrine pancreatic protein in Alzheimer's
disease and the developing human brain.";
J. Clin. Invest. 86:1004-1013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96256285; PubMed=8654365;
Bertrand J.A.; Pignol D., Bernard J.-P., Verdier J.-M., Dagorn J.-C.,
Fontecilla-Camps J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "What function for human lithostathine?: structural investigations by three-dimensional structure modeling and high-resolution NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DEVELOPMENTAL STAGE: HIGH EXPRESSION LEVELS IN FETAL AND INFANT
BRAINS; MUCH LOWER IN ADULT BRAINS.
-!- DISBASE ALZHEINER'S DISBASE AND DOWN'S SYNDROME PATIENTS SHOW
ENHANCED EXPRESSION OF PSP-RELATED TRANSCRIPTS AND INTRANBURONAL
ACCUMULATION OF PSP-LIKE PROTEINS IN THEIR BRAINS.
-!- SIMILARITY: CONTAINS 1 C-type lectin family domain.
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Crystal structure of human lithostathine, the pancreatic inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.30 ANGSTROMS) OF 23-166.
MEDLINE=20092874; PubMed=10625646;
Gerbaud V., Pignol D., Loret E., Bertrand J.A., Berland Y.,
Fontecilla-Campa J.C., Canselier J.P., Gabas N., Verdier J.M.;
"Mechanism of calcite crystal growth inhibition by the N-terminal undecapeptide of lithostathine.";
J. Biol. Chem. 275:1057-1064(2000).
                                                                                                                                                                                                                                                                                Itoh T., Tsuzuki H., Katoh T., Teraoka H., Matsumoto K., Yoshida Terazono K., Watanabe T., Yonekura H., Yamamoto H., Okamoto H.; "Isolation and characterization of human reg protein produced in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spectroscopy.";
Protein Eng. 9:949-957(1996).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBOMATE PRECIPITATION: MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.
-!- TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS AND, IN LOWER
Rouimi P., Bonicel J., Rovery M., de Caro A.; "Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreatic stone protein."; FEBS Lett. 216:195-199(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97120677; PubMed=8961348; Patard L., Stoven V., Gharib B., Bontems F., Lallemand J.-Y., de Reggi M.;
                                                                                                                                                                           "The human reg gene encodes pancreatic stone protein.";
Biochem. J. 260:622-623(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS)
                                                                                                                                                                                                                                                            MEDLINE=91032149; PubMed=2226837;
                                                                                                             IDENTITY OF REG WITH PSP.
MEDLINE=89350859; PubMed=2764894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of stone formation.";
EMBO J. 15:2678-2684(1996).
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                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 272:85-88(1990)
                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEVELS, IN BRAIN.
                                                                                                                                                                                                                                           DISULFIDE BONDS
                                                                                                                                                         Stewart T.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | | :: | | :: | | :: | | :: | : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
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MEDLINE=93176807; PubMed=7679928;
Itoh T., Teracka H.;
"Cloning and tissue-specific expression of cDNAs for the human and mouse homologues of rate pancreatitis-associated protein (PAP).";
Biochim. Biophys. Acta 1172:184-186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIŠSUB=Pancreas;
MEDLINE=93107309; PubMed=1469087;
Orelle B., Keim V., Masciotra L., Dagorn J.-C., Iovanna J.-L.;
"Human pancreatitis-associated protein. Messenger RNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL)
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    -!- SIMILARITY: Contains 1 C-type lectin family domain.

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C-TYPE LECTIN (LONG FORM)
N-LINKED (GLCNAC. . .) (P
BY SIMILARITY.
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28B89FF12C136EA3 CRC64;
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34.3%; Pred. No. 2.5e-15;
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PAP OR PAPI OR HIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PRCREATITSAP.
SMART; SMO034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
Lectin; Signal; Glycoprotein.
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HSSP, P20693, ILLJ.
INTERPRO IPRO01304, Lectin C.
InterPro, IPR003990, Pancreatis_ac.
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153 DEHCDQKFPFICKY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 34.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
65
156
172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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Q06141;
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         SOUTH THE TENT OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 NMNSG-NLVSVLTQAEGAFVASLIKESGTDDFN-VWIGLHDPKKNRRWHWSSGSLVSYKS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pleurodeles lectin.";
Eur. J. Biochem. 213:901-907(1993).
-!- FUNCTION: MAY BE INVOLVED IN PROTECTION OF EGGS AND EMERYOS
AGAINST MICROORGANISMS. CALCIUM-DEPENDENT LECTIN WITH SPECIFICITY
TO D-GLUCOSE AND D-GLUCOSAMINE. CAN AGGLUTINATE MICROORGANISMS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Signal; AlZheiner's disease; Down's syndrome; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: ANTERIOR PART OF OVIDUCT.
MISCELLANEOUS: PROTEIN SYNTHESIS INCREASES SIGNIFICANTLY UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae,
                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0008284; P:positive regulation of cell proliferation; TAS.
InterPro; IPR001353; Antifreezell.
InterPro; IPR001394; Lectin_C.
InterPro; IPR0013990; Pancreatis_ac.
Pfam; PP00059; lectin_c; 1.
PRINTS; PR0156; NUREATITSAP.
PRINTS; PR00156; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 25.7%; Score 225.5; DB 1; Length 166; Similarity 31.5%; Pred. No. 1.2e-15; S1; Conservative 30; Mismatches 62; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HETERODIMER (PROBABLE).
SUBCELLULAR LOCATION: SECRETED INTO THE INNER LAYER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tiffoche C., Chesnel A., Jego P., le Pennec J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 WGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 21-34 AND 28-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 AA
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MEDLINE=93279340; PubMed=8504829;
EMBL, JO5412; AAA3659.1; -.
EMBL; AF17231; AAD51330.1; -.
EMBL; BC005350; AAH05350.1; -.
PIR; A35197; RGHUIA.
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(Rel. 29, Last seg
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                                                                                                                                                             PIR; A45751; A45751.
PDB; 1LIT; 11-JAN-97.
PDB; 1QDD; 24-JAN-01.
Genew; HGNC:9951; REGIA.
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                                                                                                                                                                                                                                                                                                                                                      167770;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                     Genew; ]
MIM; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
    DAR WAY DOR BOOK TANK THE PROPERTY OF THE PROP
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Pred. No. 3.6e-15;

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                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC INFLAMMATION.
-!- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS AND IN SOME PATIENTS WITH CHRONIC PANCREATITIS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                              Genomics 19:108-114(1994).
-!- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
BACTERIAL PROLIFERATION.
-!- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                               Dusetti N.J., Frigerio J.M., Fox M.F., Swallow D.M., Dagorn J.C.,
                                                                                                                                                                                                                                                               "Molecular cloning, genomic organization, and chromosomal localization of the human pancreatitis-associated protein (PAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Lectin; Inflammatory response; Acute phase.

SIGNAL

1 26 BY SIMILARITY.

CHAIN

DOMAIN

38 173 C-TYPE LECTIN (LONG FORM).

DISULFID

40 51 BY SIMILARITY

DISULFID

146 163 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                   PANCREATIC ACINAR CELLS.
-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
EXPRESSION IS FOUND IN HEALTHY PANCREAS.
                                                                                   MEDLINE=92386513; PubMed=1325291;
Lasserre C., Christa L., Simon M.T., Vernier P., Brechot C.;
"A novel gene (HIP) activated in human primary liver cancer.";
Cancer Res. 52:5089-5095(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTD -> VH (IN REF. 2).
C51149FAC22EB68C CRC64;
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G0:0005615; C:extracellular space; TAS.
G0:0005525; C:soluble fraction; TAS.
G0:0005530; F:lectin; TAS.
G0:0007155; P:cell adhesion; TAS.
G0:0008283; P:cell proliferation; TAS.
G0:0007275; P:development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
expression in pancreatic diseases.";
                  Clin. Invest. 90:2284-2291(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                            MEDLINE=94245143; PubMed=8188210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D13510; BAA02728.1; --
EMBL; M8437; AAA36415.1; --
EMBL; S5176; AAB34642.1; --
EMBL; X68441; CAA48605.1; --
EMBL; L15533; AAA60020.1; --
PIR; A49616; A49616.
HSSP; P05451; 1QDD.
Genew; HGNC:8601; PAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin_c; l. PRINTS; PR01504; PNCREATITSAP.
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Iovanna J.L.
                                                                                                                                                                                          rissue=Blood
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25.2%; Score 221; DB 1; Length 175;

Query Match

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                          7;
                                                                                                                                                      63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                              3 SG-NLVSVLSGAEGSFVSSLVKSIGNSYSYVWIGLHDPTQCTEPNGEGWEWSSSDVMNYF 131
                                                                                            10 LLLSCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECOSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION SECTION 266:352-358 (1999).
-!- FUNCTION: GALACTOSE-BINDING PROTEIN WHICH RECOGNIZES SPECIFIC CARBOHYDRATE STRUCTURES AND AGGLUTINATE A VARIETY OF ANIMAL CELLS BY BINDING TO CELL-SURFACE GLYCOPROTEINS AND GLYCOLIPIDS. MAY BE CALCIUM-DEPENDENT LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: Met-33 has been shown to be oxidized to methionine sulfoxide (Ref.2) but this probably results from sample treatment prior to mass spectrometry.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ku Q., Wu X.-F., Xia Q.-C., Wang K.-Y.; "Cloning of a galactose-binding lectin from the venom of Trimeresurus
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIŜSUE-Venom;
PubMed=10561575;
Zeng R., Xu Q., Shao X.-X., Wang K.-Y., Xia Q.-C.;
Zenaracterization and analysis of a novel glycoprotein from snake
"Characterization and analysis of a novel glycoprotein from snake
venom using liquid chromatography-electrospray mass spectrometry and
Edman degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYDRATE-LINKAGE SITE, AND STRUCTURE OF CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MASS SPECTROMETRY: MW=17924.2; MW_ERR=2.4; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Galactose-binding lectin precursor (TSL).
Trimeresurus stejnegeri (Chinese green tree viper).
Trimeresurus stejnegeri (Chinese green tree viper).
Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi; Viperidae; Crotalinae; Trimeresurus.
Viperidae; Crotalinae; Trimeresurus.
                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SEQUENCE OF 24-53, AND MASS SPECTROMETRY
                            64; Indels
                                                                                                                                                                                                                                            117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
                                                                                                                                                                                                                                                                    132 AWERNPSTISSPGHCASLSRSTAFLRWKDYNCNVRLPYVCKF 173
                                                                                                                                                                                                                                                                                                                                                                                              PRT; 158 AA
32.7%; Preα. ν.ν. -
tive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlycoSuiteDB; Q9YGP1; -.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99348038; PubMed=10417338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 341:733-737(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF119097; AAD17252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin c; 1.
                            53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
    Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P22897; 1EGG
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70 ILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNK- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GALACTOSE-BINDING LECTIN.
C-TYBE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (HIGH MANNOSE).
/FIIGH-CAR_000165.
WW; 2077BC62B7A08FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
24.9%; Score 218.5; DB 1; Length 158;
Best Local Similarity 33.3%; Pred. No. 5.7e-15;
Matches 50; Conservative 19; Mismatches 72; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 --HCAEMSSNNNFLTWSSNECNKROHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 KEFCVELVSLTGYHRWNDQVCESKNSFLCQ 155
PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C.TYPE LECTIN 1; 1.
PROSITE; PS50041; C.TYPE LECTIN 2; 1.
Lectin; Signal; Calcium; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 AA;
                                                                                                                                                                                                                             SIGNAL
CHAIN
DOMAIN
DISULFID
DISULFID
DISULFID
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CARBOHYD
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         DRANGE THE TEST OF THE TEST OF
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Search completed: December 31, 2003, 09:12:10 Job time : 39 secs

Olden And B Joyd Sittle

Sequence

Seguence

Sequence

Sequence 2, Appli Sequence 1, Appli Sequence 9, Appli Sequence 6, Appli Sequence 6, Appli Sequence 1, Appli

Sequence 11, P Sequence 10, P Sequence 9, Ap

Sequence Sequence

Sequence

Sequence Sequence

Sequence:

Run on:

Searched:

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US-09-016-434-1186
5180808-1
US-09-591-435-11
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US-09-591-435-9
US-09-60-1128-0
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US-08-822-261-2
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PCT-USSS-03142-1
US-09-146-969-3
US-08-402-166-1
US-08-709-662-1
US-08-778-156-1
US-09-111-470-9
US-09-111-470-9
US-08-156-8
US-08-422-166-1
US-08-111-470-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-729-103-2
| Sequence 2, Application US/08729103
| Patent No. 5837841
| GENERAL INFORMATION:
| APPLICANT: Gold, Surya K.
| TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                      US-09-146-969-2
US-09-226-852-6
US-08-454-557C-32
US-08-340-426D-32
US-08-450-673C-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VERSION 1.5
CURRENT APPLICATION NUMBER:
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BILLINGS, LUCY J.
REGISTRATION UNMBER: 36,749
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       186.5
185.5
185.5
185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173.5
172.5
171.5
170.5
168.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
153.5
153
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-MODEL=frame+ p2n, model - DEV=xlp
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-DG=1602_21/USPTO spool p/US09525041/runat_31122003_091150_11891/app_query.fasta_1.327
-DG=1602_21/USPTO spool p/US09525041/runat_sin_-MINEMACH=0.1 - LOOPCL=0
-LOOPEXT=0 - UNITS=bits - STRAT=1 - SND=1 - MATRIX-blosume2 - TRANS-human40.cdi
-LIST-45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=bloome3 - MAXLRN=100
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-USREALCAL - OUTPWT=pto - NORM=ext - HEAPSIZE=500 - MINLENE 0 - MAXLRN=20000000
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-NORM-APP - LARGEQÜERY - NEG-SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
-DEV TIMEOUT=10 - WARN TIMEOUT=30 - THRAPAS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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6, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 5, A Sequence 5, A
                                                                                                                                                                                                                                                                                                          1 MASRSMRLLLLLSCLAKTGV.....LTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2,
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Sequence 3
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lssued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
   /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-729-103-2
US-08-468-413-1
US-09-162-508-1
PCT-US95-07169-1
US-09-146-969-1
US-08-822-261-5
US-07-778-156-4
US-07-778-156-4
US-07-778-156-4
US-07-778-156-4
US-07-778-156-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                  0.5
0.5
0.0
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                             US-09-525-041-2
878
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Match
                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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218
218
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Result

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PRIOR APPLICATION 1935
PRIOR APPLICATION NUMBER:
FILIND DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGIGSTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3256
TELEFRHOME: 201-994-1700
TELEFAK: 201-994-1700
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
   CURRENT APPLICATION DATA
                      APPLICATION NUMBER:
FILING DATE: 06 JUI
CLASSIFICATION: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCAGCACCATAGCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GluTyrIleSerGlyTyrGlnArgSerGlnProlleTrpIleGlyLeuHisAspProGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 recrargerractricaceaaccreaceacrecricarecceaecreacrererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regagcagcaacgaargcaacaaggcccaacacrrccrgrgcaagraccgacca 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08468413

Patent No. 5861494

GENERAL INFORMATION:
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: CRAELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: ROSELAND
CITT. ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                       US-09-525-041-2 (1-158) x US-08-729-103-2 (1-614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOPTWARE: WORD PERFECT 5.1
; LENGTH: 614 base pairs
; TYPE: nucleic acid
; STRANDENESS: aingle
; TOPOLGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: COLNFET02
; CLONE: 1310334
US-08-729-103-2
                                                                                                                                                                                                         7e-100
878.00
100.00$
100.00$
                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-413-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 AAGAGGCAGCAGTGGCAGTGGATTGATGGGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
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                                                                                                                                                                                                                                                                                                                                                                                                                        111 ATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAAGAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAATAACTTTTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 TGGAGCAGCAACGAATGCAACAAGGGCCAACACTTCCTGTGCAAGTACCGACCA
                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09162508
Patent No. 6080722
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                      US-09-525-041-2 (1-158) x US-08-468-413-1 (1-1114)
                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                              1.71e-99
878.00
100.00%
100.00%
LENGTH: 1114 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                             MOLECULE TYPE: CDNA
                                                                       TOPOLOGY: LINEAR
                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                     Alignment Scores:
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231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetalaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                         141 TrpSerSerAsnGluCysAsnLysArgGlnH1sPheLeuCysLysTyrArgPro
                                                                                                                                                                                                                                       Sequence 1. Application PC/TUS9507169
GENERAL INFORMATION:
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CACCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07169
FILING DATE: 06 JUN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: FERRANC, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERRICE/DOCKET NUMBER: 325
TELECHMUNICATION INFORMATION:
TELEPHONE: 201-994-1740
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER/STICS:
SEQUENCE CHARACTER/STICS:
SEGUENCE CHARACTER/STICS:
SEGUE
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878.00
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STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCT 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 GAGTACATAAGTGGCTATCAGAGAAGCCAGCGATATGGATTGGCCTGCACGACCCACAG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 AAGAGGCAGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470
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Matches:
Conservative:
Mismatches:
Indels:
                                     AIN, GILFILLAN,
OLSTEIN
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                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/09/162,508
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,413
FILING DATE: 06 JUN 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
RECISTRATION NUMBER: 335800-447
FELECOMMUNICATION INFORMATION:
TELEFONE : 201-994-1700
TELEFAX: 201-994-1700
                              ADDRESSEE: CARELLA, BYRNE, BAIN,
ADDRESSEE: CECCHI, STEWART & OLS?
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                              ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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100.00%
100.00%
CORRESPONDENCE ADDRESS:
                                                                                                                                        CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
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Best Local Similarity:
Query Match:
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APPLICANT: Iovanna, Juan-Lucio
APPLICANT: Iovanna, Juan-Charles
APPLICANT: Dagorn, Jean-Charles
APPLICANT: Barles, Jean-Charles
APPLICANT: Sarles, Jacques
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Disease (as amended).

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                        ZIP: 22040-3487

ZIP: 22040-3487

COMPUTER READABLE FORM:
MEDIUM-TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-406-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MITCHY JUNGER: 28,977
REFERENCE/DOCKET NUMBER: 2121-107P
TELECHMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "human
             Sequence 1, Application US/08464637
Patent No. 5834214
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-205-8050
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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221.00
50.62%
32.72%
25.17%
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 43..567
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Pred. No.:
JS-08-464-637-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
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                                                                                                                                             121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
                                                                                                                                                                                 530
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                                  351 GAGTACATAAGTGGCTATCAGAGAAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 CGGATCAGCTGCCCAGAAGGCACCAATGCCTATCGCTCCTACTGCTACTACTTAATGAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrp-----SerGlyLysSer 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 MetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThrTrpSer 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AGTGTTAATCCTGGCTACTGTGTGAGCCTGACCTCAAGCACAGGATTCCAGAAATGGAAG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsnCysTyrGlyTyrPheArg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                             411 AAGAGGCAGCAGTGGCAGTGGATTGATGGGGCCCATGTATCTGTACAGATCCTGGTCTGGC
                                                                      101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
                                                                                                                                                                                 471 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 LysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGlyAsnGlyAlaHis
                                                                                                                                                                                                                   141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                                         531 TGGAGCAGCAACGAATGCAACAAGCGCCAACACTTCCTGTGCAAGTACCGACCA 584
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                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09146969;
Patent No. 628858;
GENERAL INFORMATION:
TAPLICANT: Dieckgraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury;
FILE REFERENCE: 04255.75314;
CURRENT APPLICATION NUMBER: US/09/146,969
CURRENT FILING DATE: 1998-09-04;
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777
45
26
58
6
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Matches:
Conservative:
Mismatches:
Indels:
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224.00
52.59%
33.33%
25.51%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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LENGTH: 777
                                                                                                                                                                                                                                                                                           RESULT 5
US-09-146-969-1
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79 ATGCTGCTTTCCTGCCTCATGCTGCTCTCAGGTTCAAGGTGAAGAACCCCAGAGGGAA
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pancreatitis-associated protein"
/note= "see, Fig. 3"
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233
164
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::: || || :: || || 336 GGCACCGAATGGAGAAGGTTGGAGTAGCAGTGATGATTACTTT 435
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Matches:
Conservative:
Mismatches:
Indels:
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                                 ATTORNEY DATE:

NAME: Billings, Lucy J.

REGISTRATION UNMBER: 36,749

REGISTRATION UNMBER: 9F-0251 US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 797 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-778-156-4; Sequence 4, Application US/07778156; Patent No. 5436169; Patent INFORMATION:
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221.00
50.62%
32.72%
25.17%
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556 AAGTTC 561
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Best Local Similarity:
                                                                                                                                                                                                            TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 262368
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                                                                                                                                                                                                                                                                     US-09-226-852-5
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DB:
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274 GTGAAGAGCATTGGTAACAGCTACTCATACGTCTGGATTGGGCTCCATGACCCCACACAG 333
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                                                                                                                                    PROTEIN ASSOCIATED WITH ACUTE PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE PANCREATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                            : OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
2: P.C.
1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTINIED TO THE TOTAL 
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Mismatches:
Indels:
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NAME: Oblon, No. 5436169man F.
REGISTAATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
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                                                                                                      DAGORN, JEAN-CHARLES
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TELEPHONE: (703)521-4500
TELEX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIERISTICS:
IOVANNA, JUAN-LUCIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218.00
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TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
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US-07-778-156-4
                                          APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN
TITLE OF INVENTION: PRO-
TITLE OF INVENTION: PAN-
TITLE OF INVENTION: PAN
                                                            CEIM, VOLKER
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Best Local Similarity:
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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117 SerTrp-----SerGlyLysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSer 134
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Patent No. 6492499
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
ITILE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
                                                                                                                                                                                                US-09-525-041-2 (1-158) x US-08-822-261-5 (1-797)
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50.62%
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                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                        Alignment Scores:
Pred. No.:
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STATE: CACOUNTRY:
    JS-08-822-261-5
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                                    199 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGCAGATCTGGCCTGCCGGAAAGCGGCCC 258
                                                                                                  102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
                                                                                                                                                                                                                                                           ::: |||:::||| 316 GGCACCGAAGCCCAATGGAAGAAGGTTGGAGTAGCAGTGATGAATTACTTT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                    316 GTGAAGAGCATTGGTAACAGCTACTCATACGTCTGGATTGGGCTCCATGACCCCACACAG 375
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43 GlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGly 62
                                                                             AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/0882261; Patent No. 5935813; Patent No. 5935813; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: HILLMan, Jennifer L. TITLE OF INVENTION: ROTEL HUMAN PANCEATITIS-ASSOCIATED: TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZOUNTIAN TABLE FORM:

MEDIUM TYPE: Diskette COMPUTER: BM COMPUTER: BM COMPAILE COMPUTER: DOS SOFTWARE: FASESEO for Windows Version 2.0 CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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556 AAGTTC 561
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Best Local Similarity:
Query Match:
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APPLICANT:
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                                334 GGCACCGAGCCCAATGGAGAAGGTTGGGAGTGGAGTAGCAGTGATGATTACTTT 393
                                                                      394 GCATGGGAGAGAAATCCCTCCACCATCTCAAGCCCCGGCCACTGTGCGAGACTGTCGAGA 453
                                                                                                                  SerTrp-----SerGlyLysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSer 134
                                                                                                    135 AsnAsnAsnPheLeuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCys 154
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
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Matches:
Conservative:
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APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Oblon, No. 5959086man F. REGISTRATION NUBBER: 24,618
REFERENCE/DOCKET NUMBER: 354-0.
TELECOMMUNICATION INFORMATION:
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218.00
50.31%
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nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No.:
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TISSUE TYP
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83 IleSerGlyTyrGlnArgSerGlnPro---IleTrplieGlyLeuHisAspProGlnLys 101
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                                                                                                                                                                                     37 ATGCTGCTTTCCTGCCTCTGCTGCTCTCAGGTCAAGGTGAAGAACCCCAGAGGGAA 96
                                                                                                                                                                                                                                                                                                                                                         157 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGCAGATCTGGCCTGCCAGAAGCGGCCC
                                                                                                                                                                                                                                      TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESSPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                         10 LeuLeuLeuSerCysLeu---AlaLysThrGlyValLeuGlyAspIleIleMetArg.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
Mismatches:
Indels:
Gaps:
                                                                                             US-09-525-041-2 (1-158) x US-08-422-166-4 (1-522)
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Patent No. 5436169
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : IOVANNA, JUAN-LUCIO
: KEIM, VOLKER
: DAGORN, JEAN-CHARLES
32.92%
24.83%
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MEDIUM TYPE: Floppy
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Query Match
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GTGAAGGGATTGGTAACAGCTACTCATACGTCTGGATTGGGCTCCATGACCCCACACAG
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
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23
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64
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                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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               REFERENCE/DOCKET NUMBER: 354-012-0 PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08822261
Patent No. 5935813
GENERAL INFORMATION:
24,618
                                                                                                                                                                                                                                                                                                            9.48e-18
218.00
50.31%
32.92%
24.83%
                                                                                                                          LENGTH: 798 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                        TELEKA: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                         TISSUE TYPE: pancreas
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                Alignment Scores:
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79 ATGCTGCTTTCCTGCCTCATGCTGCTGTCTCAGGTTCAAGGTGAAGAACCCCAGAGGGAA 138
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                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-(TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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50.31%
32.92%
24.83%
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TYPE: nucleic acid
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CLONE: 189600
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Best Local Similarity:
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TOPOLOGY: line
                                                                                                                                                 ZIP: 94304
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Pred. No.:
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199 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGCAGATCTGGCCTGCCAGAAGCGGCCC 258
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                                                                                                                                               43 GlyTyrPheArgLysLeuArgAenTrpSerAepAlaGluLeuGluCysGlnSerTyrGly 62
                                                                                                                                                                                                                         AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
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 10 LeuLeuLeuSerCysLeu---AlaLysThrGlyValLeuGlyAspIleIleMetArg---
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                                                                       28 ---ProSer------CysAlaProGlyTrpPheTyrHisLysSerAsnCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09146969
; Batent No. 6228585
; GENERAL INFORMATION:
; APPLICANT: Dieckgraefe, Brian K.
; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
; TITLE OF INVENTION: UMBER: US/09/146,969
; CURRENT FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARER PatentIn Ver. 2.0
; SEQ ID NO 2
LENGTH: 798
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Conservative:
Mismatches:
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Gaps:
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CORGANISM: Homo sapiens
US-09-146-969-2
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Query Match:
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135 AsnAsnAsnPheLeuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCys 154
                                                                                                                                                                                                                                   Sequence 12, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/NS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFATION: 435
PRIOR APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
FELECOMMUNICATION NUMBER: 24,618
REFERENCE/COCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base paire
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Matches:
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Indels:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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32.92%
24.83%
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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STRANDEDNESS: unknown
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Best Local Similarity:
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US-08-422-166-12
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316 GTGAAGAGCATTGGTAACAGCTACTCATACGTCTGGATTGGGCTCCATGACCCCCACACAG 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE. ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/226,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/822,261
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0251 UF
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
FELEFAX: FWATH: 798 base pairs
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Patent No. 6492499
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
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102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
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                                                                                                                                                                                                                                                                                    43 GlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGly 62
                                                                                                                                                                                                                                                                                                                                                 63 AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
                                                                                                                                                                                                                       28 ---ProSer-----CysAlaProGlyTrpPheTyrHisLysSerAsnCysTyr
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Mismatches:
Indels:
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                             Matches:
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Search completed: December 31, 2003, 10:41:06 Job time : 79 secs

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein December 31, 2003, 09:11:17; Search time 43 Seconds (without alignments) 353.364 Million cell updates/sec Run on:

US-09-525-041-2 878

1 MASRSMRLLLLLSCLAKTGV.....LTWSSNECNKRQHFLCKYRP 158 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DB	Ω	. De	Description
1	254.5	29.0	165	7	A47148	re	reg I, regeneratin
7	254.5	29.0	165	~	A28351	ed	crea
m	241.5	27.5	142	7	878596	ō.	ovocleidin - chick
4	240		166	-	RGHU1B	re	ģ
S	236.5	26.9	173	N	B47148	re	reg II, regenerati
9	236.5	26.9	174	~	183377	re	ℼ
7	233	26.5	135	7	A38609	le	lectin, galactose-
80	231	26.3	174	~	S54979	ed	ancreatitis-assoc
D	231	26.3	175	7	A37194	ed	pancreatic thread
10	228.5	26.0	174	٦	A48689	ed	pancreatitis-assoc
11	225.5	25.7	166	Н	RGHU1A	re	regenerating islet
12	224	25.5	166	~	A45751	ed	ancreatic stone p
13	222.5	25.3	172	7	S32489	ĵe	lectin - Iberian r
14	221	25.2	175	~	A49616	ed	pancreatitis-assoc
15	206.5	23.5	152	N	JC7134	_ 08	agkisacutacin alph
16	203.5	23.5	131	7	JC5058	įq	bitiscetin alpha c
17	203	23.1	175	71	A41719	BQ	pancreatic stone p
18	202.5	23.1	123	~	JC2415	o e	eta ch
19	202.5	23.1.	152	~	JC4690	8	coagulation factor
20	200.5	25.8	125	N	JC5059	iq	bitiscetin beta ch
21	196.5	22.4	146	~	JC7105	ag	aggretin beta chai
22	196.5	22.4	146	N	JC4691	8	coagulation factor
23	194	22.1	175	N	S29822	BO	pancreatitis-assoc
24	193	22.0	330	N	T46256	īď	brevican - human (
	193	22.0	912	N	A54423	īq	brevican precursor
56	191	ä	883	N	857653	īd	brevican precursor
27	189	21.5	133	~	A47267	ğ	botrocetin alpha c
28	185.5	21.1	125	~	B47267	oq	botrocetin beta ch
29	185.5	21.1	129	~	JC4329	S	

Dancreatic stone protein precursor - rat

NyAlternate names: lithostathine
C;Species: Rattus norvegicus (Norvey rat)
C;Species: Rattus norvegicus (Norvey rat)
C;Date: 31.Mar-1990 #sequence revision 31-Mar-1990 #text_change 11-May-2000
C;Accession: A28351; A39081; PL0147; S34618
R;Terazono, K.; Yamamoto, H.; Takssawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto
R;Terazono, K.; Yamamoto, H.; Takssawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto
A;Reference number: A32704; MUD:88115343; PMID:2963000
A;Reference number: A2704; MUD:88115343; PMID:2963000
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-165 <TER>

brevican precursor	neurocan precursor	agkisacutacin beta	asialoglycoprotein	aggretin alpha cha	hepatic lectin Hl	chondroitin sulfat	neurocan - mouse	versican precursor	versican precursor	asialoglycoprotein	lectin BRA3-1 prec	lectin BRA3-2 prec	versican precursor	versican precursor	coagulation factor
S49126	S28764	JC7135	S13165	PC7027	LNHU1	A47171	S52781	A55535	A60979	LNHU2A	LNRC1	LNRC3	T14274	T42389	B42972
0	~	N	~	(7	٦	~	~	-	٦	٦	-	٦	~	~	~
83	1257	146	301	144	291	3562	1268	2397	2409	311	162	162	1643	3381	123
80	_														
	•••	21.0	20.8	20.7	20.6	20.6	20.4	20.4	20.4	20.3	20.2	20.2	20.2	20.2	19.6
21.1	21.1												177 20.2		

ALIGNMENTS

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reg 1, regenerating islet cells - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000
C;Accession: A47148
B;Unno, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; Oke J. Bold. Chem. 268, 15974-15982, 1993
A;Title: Structure, chromosomal localization, and expression of mouse reg genes, reg I ar A;Reference number: A47148; MUID:93340209; PMID:8340418
A;Reference number: A47148
A;Status: preliminary
A;Molecule type: DNA
A;Status: 1-165 < UNN>
A;Cross-references: GB:D14010; NID:g391771; PIDN:BAA03111.1; PID:g391772
C;Genetics:
A;Introns: 21/1; 60/3; 106/3; 144/A
C;Superfamily: tetranectin; C-type lectin homology
F;35-161/Domain: C-type lectin homology < LCH>
F;35-46,63-161,136-153/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 DLFCQNMNSG-YLVSVLSQAEGNFVASLIKESGTTDAN-VWTGLHDPKRNRRWHWSSGSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 BLECOSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWIDGAM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLSCLAKTGVLGDIIMRP-----SCAPGWFYHKSNCYGYFRKLRNWSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 YLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.0%; Score 254.5; DB 2 Best Local Similarity 31.1%; Pred. No. 6.6e-18; Matches 52; Conservative 35; Mismatches 51
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us-09-525-041-2.rpr

Length 142;

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27.5%; Score 241.5; DB 2; 33.8%; Pred. No. 1.1e-16;
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A;Map position: 2p12-2p12
A;Introns: 22/1; 61/3; 107/3; 145/1
                                                                                                                                                                                                                                                                                                                                                               140 TWSSNECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                   :|:: | :| |:||
124 SWAARPCTERNAFVCK 139
                                                                46; Conservative
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Best Local Similarity
Matches 46; Conserv
                              Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:REG1B; REG1
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      Query Match
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F;35-161/Domain: C-type lectin homology <LCH>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
A;Cross-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605
R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D.
Siol. Chem. 266, 786-791, 1991
A;Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocra A;Reference number: A39081; MUID:91093273; PMID:1985964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209
C;Comment: This protein is found in pancreatic calculi of mammals. A peptide bond betwee
rotein into an insoluble protein at a neutral pH of 5.5 to 7.5.
                                                                                                                                                                                                                                     J.Residues: 1-165 <ROU>
J.Residues: 1-165 <ROU>
J.Cross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463
J.Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M.
J. Dechem. Physiol. B 93, 793-797, 1989
J.Title: Characterization in rat pancreatic juice of a protein homologous to the human J.Reference number: PLO147; MUID:90031455; PMID:2680252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.
Cochim. Biophys. Acta 1174, 99-102, 1993
Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.
Reference number: S34618; MUID:93326645; PMID:7916640
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C;Species: Gallus gallus (chicken)
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 20-Sep-1999
C;Accession: S78956
R;Baernholdt, D.; Andersen, S.O.
aubmitted to the Protein Sequence Database, September 1998
A;Reference number: S78596
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F;5-16,33-138,113-130/Disulfide bonds: #status experimental
F;61,67/Binding site: phosphate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: tetranectin; C-type lectin homology Keywords: pyroglutamic acid 1-21/Domain: signal sequence #status predicted <SIG>
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30.6%; Pred. No. 6.6e-18;
tive 38; Mismatches 51
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A; Residues: 1-142 - SAAE>
A; Residues: 1-160 - SAAE>
C; Superfamiental source: egg-shell
C; Superfamily: tetranectin; C-type lectin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein
Residues: 22-69 <ADR>
Experimental source: pancreas
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Best Local Similarity 30.6%
Matches 52; Conservative
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Molecule type: DNA
                                                                                                                                                                                 Status: preliminary; Molecule type: mRNA
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A, Residues: 1-166 CBAR.
A, Residues: 1-166 CBAR.
A, Cross-references: GB:L08010; NID:g307368; PIDN:AAA18204.1; PID:g487726
A, Note: this gene appears to be expressed in pancreas and liver
R; Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki, Y.; Miyashita, H.; Yone)
Biochim. Biophys. Acta 1217, 199-202, 1994
A; Title: Isolation, structural determination and expression of a novel reg gene, human re
A, Reference number: S42729; MUID:94153997; PMID:8110835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:D17291; NID:9474307; PIDN:BAA04124.1; PID:9474308; Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like cleav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Superfamily: tetranectin; C-type lectin homology
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
C;L22/Domain: signal sequence #status predicted <SIG>
F;122/Domain: signal sequence #status predicted <SIG>
F;23-166/Product: regenerating islet lectin lbeta #status predicted <MAT>
F;34-166/Product: pancreatic stone protein #status predicted <MAT>
F;34/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;23/Modified site: carbohydrate (Thr) (covalent) #status predicted
F;33-34/Cleavage site: Arg-Ile (trypsin) #status predicted
F;36-47,64-162,137-154/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: reg-related protein; reg1-beta protein
N;Contains: pancreatic stone protein (PSP)
N;Contains: pancreatic stone protein (PSP)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 834591; 842729; Ā44712
C;Accession: 634591; 842729; Ā44712
FFBS Lett. 327, 289-293; 1993
A;Title: A gene homologous to the reg gene is expressed in the human pancreas.
A;Reference number: 834591; MUID:93351647; PMID:8348956
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                                                                                                                                                                                                                                                      84 --SGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSW--SGKSMGGNKHCAEMSSNNNFL 139
                                                                                                                                                                                                                                                                                                          97 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSS 143
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                                                                                  30 CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI-----
    Gaps
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    11;
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    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regenerating islet lectin 1-beta precursor - human
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us-09-525-041-2.rpr

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Gispeciaes: Rattus norvegicus (Norway rat)
Cispeciaes: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999
Ciscession: Si4979; Si49438
Ribusetti, N.J.; Frigerio, J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna, J.L.
Blochem. J. 307, 9-16, 1995
A;Title: Cloning, expression and chromosomal localization of the rat pancreatitis-associaty. Reference number: S54979; MUD:95234061; PMID:7717998
A;Reference number: S54979; MUD:95234061; PMID:7717998
A;Reference number: S54979; MUD:9483931; PIDN:AAA79231.1; PID:9483932
A;Reference number: SA979
A;Reference number: S4979; MUD:9483931; IJ993
A;Reference number: S49438; MUD:94060113; PMID:8241280
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                                                                                                                                                                                            95 VNNNQDIWIGLHDPTMGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEP 154
                                                                                                                                                           86 YORSOPIWIGLHDPOKROO-----WOWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 SQP-IWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GQENVWIGLRDKKKDPSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLWNDQ 121
                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | ::| || |::| |::| |::| |::| 36 RISCPMGSKAYRSYCYTLVTTLKSWPQADLACQKRPSG-HLVSILSGGBASFVSSLVTGR
                                                      27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
     9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
26.5%; Score 233; DB 2; Length 13
Best Local Similarity 34.4%; Pred. No. 7.2e-16;
Matches 45; Conservative 18; Mismatches 64; Indels
     56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactose-specific - western diamondback rattlesnake
     49; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                 139 LTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                  155 LKWGDHHCDVELPFVCKPK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ECNKROHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VCESKDAFLCQ 132
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A;Molecule type: mRNA
A;Residues: 1-174 <FRI>
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     Matches
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Cispecies Rattus norvegicus (Norway rat)
Cjaccesion: 160296; Ba377
CjAccesion: 160206; Ba3377
CjAccesion: 160206; Ba3377
CjAccesion: 160206; Ba3377
CjAccesion: 160206; Ba3377
CjAccesion: 160206; MUD: 94314238; PMID: 8039722
A;Title: Structure and expression of a novel rat RegIII gene.
A;Reference number: 160296; MUD: 94314238; PMID: 8039722
A;Accession: 160296
A;Accession: 160296
A;Accession: 160296
A;Accession: 160296
A;Accession: 183377
A;Accession: 183377
A;Accession: 183377
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                                                                                                                                                                                                                          regili, regenerating islet cells - mouse
Cispecies: Mus musculus (house mouse)
Cjate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000
CjAccession: B47148
Ribmo, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; O.
J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, chromosomal localization, and expression of mouse reg genes, reg I.A;Reference number: A47148; MUID:93340209; PMID:8340418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 LRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQW 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RLTWGEADLFCQNM-NAGHLVSILSQAESNFVASLVKESGTTASN-VWTGLHDPKSNRRW 118
92 STDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASRSMRLLLLLSCLAKTGVLGDII-------MRPSCAPGWFYHKSNCYGYFRK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQNNVYLILFLCLMFLSYSQGQVAEEDFPLAEKDLPSAKINCPEGANAYGSYCYYLIED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-173 <UNN>
A;Cross-references: GB:D14011; NID:g391773; PIDN:BAA03112.1; PID:g391774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 QWIDGAMYLYRSWS--GKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: D26078; NID: 9471159; PIDN: BAA05071.1; PID: 9471160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%; Score 236.5; DB 2; Length 173; 28.7%; Pred. No. 4.2e-16; ive 33; Mismatches 72; Indels 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Introns: 22/1; 68/3; 114/3; 152/1
C;Superfamily: tetranectin; C-type lectin homology
E;43-169/Domain: C-type lectin homology <LCH>
E;43-169/Domain: C-type lectin homology <LCH>
E;43-54,71-169,144-161/Disulfide bonds: #status predicted
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C;Superfamily: tetranectin; C-type lectin homology
F;39-170/Domain: C-type lectin homology <LCH>
                                                 144 NECNKROHFLCKYR 157
                                                                                                     152 ESCEKKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 28,74
Matches 50; Conservative
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Best Local Similarity
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A; Residues: 1-174 <RE2>
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Rivigario, J.M.; Dusetti, N.J.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
Biochemistry 32, 9236-9241, 1993
A;Title: Identification of a second rat pancreatitis-associated protein. Messenger RNA c]
A;Reference number: A48689; MUID:93378971; PMID:8369291
A;Accession: A46689
A;Ketauts: preliminary
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-174 <FRI>
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A, Residues: 23-52;160-166 <ITO>
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Best Local Similarity
Matches 48; Conserv
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R;de la Monte, S.M.; Ozturk, M.; Wands, J.R.
C. Clin. Invest. 86, 1004-1013, 1990
A;Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease an A;Reference number: A37194; WUID:90368981; PMID:2394826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein

A; Mesidues: 38-138;141-175 <CAI>

C; Comment: The purified protein undergoes a reversible globule-fibril transformation and

C; Superfamily: tetranfectin; C-type lectin homology

C; Keywords: disulfide bond; extracellular protein; pancreas

F; 38-138/Product: pancreatic thread protein chain A #status experimental <ACH>

F; 40-171/Domain: C-type lectin homology <LCH>

F; 141-175/Product: pancreatic thread protein chain B #status experimental <BCH>
A;Cross-references: GB:L20869; GB:S67496; NID:g463279; PIDN:AAA41809.1; PID:g463280
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                                                                                                                                                                                                                                                                                                                                                                                                      ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || :| || || || || || || 65 DLACQKRPSG-HLVSVLSGSEASFVSSLIKKSSGNSGQNVWIGLHDPTLGQEPNRGGWEWS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 SYGNGAHLASILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQ-----WQWIDGAMY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 KRPSG-HLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSBANAGGWEWISNDVL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic thread protein precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
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                                                                                                                                                                                                                                  Gaps
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;Residues: 1.175 <DEL>
;Cross-references: GBL>
;Cross-references: GBLS9794; NID:g163648; PIDN:AAA30750.1; PID:g163649
;Cai, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabb, J.W.
Protein Chem. 9, 623-632, 1990
;Title: Structural analyais of bovine pancreatic thread protein.
;Reference number: A53897; MUID:91197388; PMID:2085387
                                                                                                                                                                Query Match 26.3%; Score 231; DB 2; Length 174; Best Local Similarity 32.4%; Pred. No. 1.5e-15; Matches 55; Conservative 28; Mismatches 73; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 NADVMNYFNWETNPSSVSGSHCGTLTRASGFLRWENNCISELPYVCKFK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%; Score 231; DB 2; Length 175; 30.9%; Pred. No. 1.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62; Indels
                                                     A;Introns: 26/1; 65/3; 111/3; 153/1
C;Superfamily: tetranectin; C-type lectin homology
F;40-170/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches
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Matches
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A48689
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panoreatitis-associated protein PAP-2 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

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N'Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; regl-al N'Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; regl-al N'Contains: pancreatic stone protein (PSP)
C'Ordains: pancreatic stone protein (PSP)
C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Spacies: Har-1990 #sequence revision 03-Aug-1995 #text_change 08-Dec-2000
C'Accession: A35197; B28351; $12950; S02767; S02419; S00113; S01471; A25246
R'Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 265, 7432-7439, 1990
A; Fitle: Complete nucleotide sequence of human reg gene and its expression in normal and product of the gene.
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A;fitle: N-terminal sequence extension in the glycosylated forms of human pancreatic stor A;Reference number: S02767; MUID:89150292; PMID:2493268
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A;Residues: 1.166 cWAT.
A;Residues: 1.166 cWAT.
A;Cross-references: GB:J05412
B;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto B. Biol. Chem. 23, 2311.2114. 1988
A;Title: A novel gene activated in regenerating islets.
A;Reference number: A92704; MUID:88115343; PMID:2963000
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A; Residues: 1-166 <TRR>
A; Residues: 1-166 <TRR>
A; Cross-references: GB:M18963; NID:g190978; PIDN:AAA36558.1; PID:g190979
A; Cross-references: GB:M18963; NID:g190978; H.; Matsumoto, K.; Yoshida, N.; Terazono, BEBS Lett. 272, 85-88, 1990
FEBS Lett. 272, 85-88, 1990
A; Title: Isolation and characterization of human reg protein produced in Saccharomyces A; Reference number: $12950; MUID:91032149; PMID:2226837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 VNNNODIWIWIHDPTMGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                36 RISCPMGSKAYRSYCYTLVTTLKSWFQADLACQKRPSG-HLVSILSGGEASFVSSLVTGR
                                                                                                                                                                                                                                                                                                                                                                                               27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                       Gaps
A,Cross-references: GB:L10229; NID:g409014; PIDN:AAA02980.1; PID:g409015 CS.Superfamily: tetranectin; C-type lectin homology E;39-170/Domain: C-type lectin homology <LCH> F;39-50,67-170,145-162/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                   Score 228.5; DB 1; Length 174; Pred. No. 2.6e-15;
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                                                                                                                                                                                                                                                                                                              57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product of the gene.
A;Reference number: A35197; MUID:90237042; PMID:2332435
A;Accession: A35197
                                                                                                                                                                                                                   ch 26.0%; Score 228.5; I
1 Similarity 34.5%; Pred. No. 2.6e
48; Conservative 25; Mismatches
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FEBS Lett. 229, 171-174, 1988
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16

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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000
C;Date: 20-Feb-1995 #sequence revision, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
R;Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
A;Title: Molecular cloning, genomic organization, and chromosomal localization of the hun
A;Reference number: A49616; MUID:94245143; PMID:8188210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S32489; S28530
R;Tiffoche, C.; Chesnal, A.; Jego, P.; le Pennec, J.P.
Bur. J. Biochem. 213, 901-907, 1993
A;Title: Isolation and characterization of a cDNA clone encoding a Pleurodeles lectin.
A;Reference number: S32489; MUID:93279340; PMID:8504829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 GYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSW--SGKSMGGNKHCAEMSSNNNFLTWS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 GTDDFN-VWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 CTPGWDCHFNSYYKYIPNAKSWTDAEFYCQKLYPGAHLASIHSEDENDFLTEITFKNNSN 96
                                                                                                                                                                                                                                                                                                                                                                                                                27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYI--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQRS
      A,Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-166 <GIO>
A;Residues: 1-166 <GIO>
A;Cross-references: GB:M27190; NID:g623412; PIDN:AAA60546.1; PID:g623413
C;Superfamily: tetranectin; C-type lectin homology
F;36-162/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-172 <TIF>
A;Residues: 1-172 <TIF>
A;Cross-references: EMBL:X69062; NID:g64257; PIDN:CAA48800.1; PID:g64258
C;Superfamily: tetranectin; C-type lectin homology
F;37-164/Domain: C-type lectin homology <LCH>
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N'Alternate names: C-type lectin; pancreatic stone protein homolog HIP
                                                                                                                                                                                                                                     Query Match 25.5%; Score 224; DB 2; Length 166; Best Local Similarity 33.3%; Pred. No. 7e-15; Matches 45; Conservative 26; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 25.3%; Score 222.5; DB Similarity 34.3%; Pred. No. 1e-14; 46; Conservative 22; Mismatches 5
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151 DVPCEDKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 SNECNKROHFLCKYR 157
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Matches 46; Conserv
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A; Residues: 1-175 < DUS>
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A map position: 2p12-2p12
A introns: 22/1; 61/3; 107/3; 145/1
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: glycoprotein; Lectin; pancreas; pyroglutamic acid
F; 1-22/Domain: signal sequence #status predicted <SIG>F; 2-16/Froduct: regenerating; slate lectin 1-alpha #status experimental <MAT>F; 34-16/Froduct: pancreatic stone protein #status experimental <MAT>F; 34-16/Froduct: pancreatic stone protein #status experimental <MAT>F; 34-16/Froduct: pancreatic stone protein #status experimental <MAT>F; 31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F; 37/Binding site: carbohydrate (Thr) (covalent) #status experimental
F; 33-34/Cleavage site: Arg.Ile (trypsin) #status experimental
F; 36-47,64-162,137-154/Disulfide bonds: #status experimental
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A;Molecule type: protein
A;Molecule type: protein
A;Mostales: 33-48 cR02-
R;Montalto, G. 19 Bonicel, J.; Multigner, L.; Rovery, M.; Sarles, H.; De Caro, A.
Biochem. J. 238, 227-232, 1986
A;Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancreat
A;Reference number: A25246; MUID:87099950; PMID:3541906
                                                                                                                                                                                                                                                                                                                            A,Accession: S00113
A,Molecule type: protein
A,Residues: 34-166 <DEL>
R,Residues: 34-166 <DEL>
R,Rouimi, P.; Bonicel, J.; Rovery, M.; de Caro, A.
FBBS Lett. 216, 195-199, 1987
A,Title: Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreati
A,Reference number: S01471; MUID:87219142; PMID:3108036
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R;Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J.; Sarles, H.; Dagorn, J.C.
J. Clin. Invest. 84, 100-106, 1989
A;Title: Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and
A;Reference number: A45751; MUID:89292148; PMID:2525567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 NMNSG-NLVSVLTQAEGAFVASLIKESGTDDFN-VWIGLHDPKKURRWHWSSGSLVSYKS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 MLISCLMFLSQSQGQEAQTELPQ---ARISCPECTNAYRSYCYYFNEDRETWVDADLYCQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LLLSCL-----AKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQ 59
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A45751
pancreatic stone protein precursor - human
C;Species: Homo Bapiens (man)
C;Species: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 28-May-1999
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31.5%; Pred. No. 5e-15;
ive 30; Mismatches 62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 W--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GDB:132455; OMIM:167770
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Matches 51; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: GDB:REG1A; REG
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Length 172;

Indels

55; DB 2;

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122 SKKCLGVHIETGFHKWENFYCEQQDPFVCE 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-175 cLAS, 1/27 cLAS, 
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;Residues: 1-175 <1,42>
;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
. Clin. Invest. 90, 2284-2291, 1992
. Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in ;Reference number: ISSS80; MUID:93107309; PMID:1469087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Verni
Ir. J. Blochem. 224, 229-38, 1994
Title: Structural organization and chromosomal localization of a human gene (HIP/PAP)
Reference number: 848197; MUID:94357229; PMID:8076648
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C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C;Accession: JC7134; PC7037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.2%; Score 221; DB 2; Length 175;
Best Local Similarity 32.7%; Pred. No. 1.5e-14;
Matches 53; Conservative 29; Mismatches 64; Indels 16; Gaps
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A;Cross-references: GDB:136839; OMIM:167805
A;Cross-references: GDB:136839; OMIM:167805
A;Cross-references: GDB:125p12
A;Introns: 25p12-2p12
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: acute phase; extracellular protein; pancreas
C;Keywords: acute phase; extracellular protein; pancreas
F;27-175/Product: pancreatitie-associated protein #status predicted <AMAT>
F;27-175/Product: pancreatitie-associated protein #status predicted <AMAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-171/Domain: C-type lectin homology <AMAT>
F;40-171/Domain: C-
;Cross-references: GB:L15533; NID:g482908; PIDN:AAA60020.1; PID:g482909; lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C. ancer Res. 52, 5089-5095, 1992.

Ancer Res. 52, 5089-5095, 1992.

?title: A novel gene (HIP) activated in human primary liver cancer.

?Reference number: A44931; MUID:92386513; PMID:1325291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ross-references: GB:D13510; NID:g285970; PIDN:BAA02728.1; PID:g285971
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Residues: 1-175 <ITO>
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R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Blochem. Blochyw. Boomun. 265, 530-535, 1999
A;Title: Purification, characterization, and CDNA cloning of a new fibrinogenlytic venom A;Reference number: JC7134; MUID:20025379; PMID:10558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 IESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEE--- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LILISCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS
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A;Accession: PC7037
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A;Rosidues: 24-53;84-86;87-94;125-136;137-152 <CH2>
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F;1-23/Domain: signal sequence #status predicted <SIG>
P;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
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31.3%; Pred. No. 3.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                                                                       A; Cross-references: GB:AF176420
A; Experimental source: venom gland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                           A; Residues: 1-152 <CHE>
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Search completed: December 31, 2003, 09:15:53 Job time : 44 secs

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Sequence:

Run on:

Searched:

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Q94GN9
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878
1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP
          GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             830525 seqs, 258052604 residues
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                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Q9D8GS
Q9D8SS
Q8NER6
Q8NER6
Q9FSNO
Q9FSNO
Q9FSNO
Q9CVF4
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Q9CVF8
Q9OWI8
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sp_virus: *
sp_virus: *
sp_vertebrate: *
sp_unclassified: *
sp_rvirus: *
sp_bacteriap: *
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungl:*
sp_fungl:*
sp_invertebrate:*
sp_mammal:*
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sp_organelle:*
sp_phage:*
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Match Length
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Database

Q8av98 trimeresuru Q9iam0 agkistrodon Q8uvc6 agkistrodon Q8aya5 agkistrodon

RESULT 1 OGBYZE DG OGBYZE AC OGBYZE AC OGBYZE DG OGGYZE DG O								
	RESU.							
•	10	Q9BYZ8	PRELIMINARY	;;	PRT;	158 AA.		
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.,,	П	01-MAR-2003	(TrEMBLrel.	. 23, Га	ist anno	tation up	odate)	
.,,	DE	Regenerating	g gene type	IV (Gas	trointe	etinal e	scretory	protein GISP)
•	DE	(REG-like p	rotein).					
· · · · · · · · · · · · · · · · · · ·	SO	Homo sapien	B (Human).					
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	႘	Mammalia; E	utheria; Pri	imates;	Catarrh	ini, Hom	inidae; H	lomo.
	ŏ	NCBI TaxID=						
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••••••	ΚX	MEDLINE=212	10973; PubMe	d=11311	.942;			
••••••	æ	Hartupee J.(C., Zhang H.	., Bonal	do M.F.	, Soares	M.B., Di	eckgraefe B.F
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Biochim. Biophys. Acta 1518:287-293(2001). [2] SEQUENCE FROM N.A. TISSUE-Colon cancer; Violette S., Festor B., Dussaulx E., Citadelle D., Chambaz J., Lacasa M., Lesuffleur T.; "The new intestinal Reg IV gene is involved in drug-resistancy colon tumor cells."; "Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. TISSUE-Colon; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [43] SEQUENCE FROM N.A. Issue (NOV-2001) to the EMBL/GenBank/DDBJ databases. [44] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RT	the human re	egenerating	protein	ı family	: Reg IV	(1).";	
[2] SEQUENCE FROM N.A. TISSUE=Colon cancer; Violette S., Festor B., Dussaulx E., Citadelle D., Chambaz J. Lacasa M., Lesuffleur T.; Lacasa M., Lesuffleur T.; "The new intestinal Reg IV gene is involved in drug-resistancy colon tumor cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. TISSUE=Colon; Strausberg N.A. Strausberg N.A. Strausberg N.A. Strausberg N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RL	Biochim. Bio	ophys. Acta	1518:28	17-293 (2	001).		
SEQUENCE FROM N.A. TISSUE=COlon cancer; Violette S., Festor E., Dussaulx E., Citadelle D., Chambaz J. Violette S., Festor E., Dussaulx E., Citadelle D., Chambaz J. Lacasa M., Lesuffleur T.; "The new intestinal Reg IV gene is involved in drug-resistance colon tumor cells." Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. **SISTUENCE FROM N.A. TISSUE=Colon; Strausberg R.;	Z.	[3]						
TISSUE=Colon cancer; Violette S., Peator B., Dussaulx E., Citadelle D., Chambaz J. Lacasa M., Lesufflaur T.; "The new intestinal Reg IV gene is involved in drug-resistancy colon tumor cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A. TISSUE=Colon; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FRO	OM N.A.					
Violette S., Festor E., Dussaulx E., Citadelle D., Chambaz J. Lacasa M., Lesuffleur T.; Lacasa M., Lesuffleur T.; "The new intestinal Reg IV gene is involved in drug-resistance colon tumor cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. 433 SEQUENCE FROM N.A. TISSUB-COLON; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [44] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RC	TISSUE=Color	n cancer;					
Lacasa M., Lesuffleur T.; "The new intestinal Reg IV gene is involved in drug-resistance colon tumor cells." Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. *31 *23 *EQUENCE PROM N.A. TISSUB=Colon; Strausberg R.; **EMDITTER TOWN-2001) to the EMBL/GenBank/DDBJ databases. **Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family. Stubmitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	Æ	Violette S.	, Festor B.,	Dussau	ilx E.,	Citadell	∍ D., Cha	mbaz J.,
"The new intestinal Reg IV gene is involved in drug-resistance colon tumor cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. 431 SEQUENCE FROM N.A. TISSUE-Colon; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; In WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	æ	Lacasa M.,]	Lesuffleur 1					
colon tumor cells."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. -{31} SEQUENCE FROM N.A. TISSUE-COLON; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RT	"The new in	testinal Reg	y IV gen	le is in	volved i	n drug-re	sistance of
. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. 43) SEQUENCE PROM N.A. TISSUB-Colon; Strausberg R.; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; Lin WC.; Inthostation of gastrointestinal secretory protein (GISP), member of lithostathine gene family. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RT	colon tumor	cells.";					
-{3} SEQUENCE PROM N.A. TISSUE=Colon; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EWBL/GenBank/DDBJ databases.	RL	.Submitted (1	FEB-2001) to	the EV	BL/GenB	ank/DDBJ	database	.00.
SEQUENCE FROM N.A. TISSUE=COLOn; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EWBL/GenBank/DDBJ databases.	RN	-{3]						
TISSUE=Colon; Strausberg R.; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family." Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FRO	OM N.A.					
Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EWBL/GenBank/DDBJ databases.	RC	TISSUE=Color	;;					
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[4] SEQUENCE FROM N.A. Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family. Submitted (APR-2000) to the EWBL/GenBank/DDBJ databases	RL	Submitted (1	NOV-2001) to	the EM	BL/GenB	ank/DDBJ	database	.00
SEQUENCE FROM N.A. Lin WC.; Lin Gentification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (APR-2000) to the EWBL/GenBank/DDBJ databases.	RN	[4]						
Lin WC.; "Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family."; Submitted (ApR-2000) to the EWBL/GenBank/DDBJ databases.	RP	SEQUENCE FRO	OM N.A.					
"Identification of gastrointestinal secretory protein (GISP), member of lithostathine gene family." Submitted (APR-200) to the EWBL/GenBank/DDBJ databases.	RA	Lin WC.;						
-	RT	"Identificat	tion of gast	rointes	tinal s	ecretory	protein	isp),
	RT	member of 1;	ithostathine	gene f	amily."		1	
	RL	Submitted ()	APR-2000) to	the EN	BL/GenB	ank/DDBJ	database	. 69

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Nature 409:685-690(2001)
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                                                                                                    rissum=Colon;
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SEQUENCE FROW N.A.

SEQUENCE FROW N.A.

A REDINE-2108560; PubMed=11217851;

KRAMI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Saburner M., Batalov S., Casavant T.,

Radota K., Matsuda W., Shourier M., Batalov S., Radotha H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Rashio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamido M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Sasaki H., Sato K., Schoenbach C., Schoguez I., Sakamoto N.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wunnblaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 878; DB 4; Length 158; 100.0%; Pred. No. 3.8e-87; ive 0; Mismatches 0; Indels
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Kamazanen M., Heiskala K., Heiskala M., Andersson L.C.;
Kamazanen M., Heiskala K., Heiskala M., Andersson L.C.;
Submitted, GUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR345934; AAK5969.1; -.
EMBL; BC017098; AAK40869.1; -.
EMBL; AF254415; AAK48435.1; -.
EMBL; AF254415; AAK48435.1; -.
EMBL; AY126670; AAM95598.1; -.
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7308849CBBD6E93E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
2010002L1SRik protein (RIKEN cDNA 2010002L15 gene).
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PRINTS; PR01504; PNCREATITSAP.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                    HSSP; P05451; 1QDD.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
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Best Local Similarity 100.03
Matches 158; Conservative
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XX STRAIN=C57BL/63; TISSUB=Small intestine;
XX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
XA Arakawa T., Shinagawa A., Shibata K., Xonno H., Adachi J., Fukuda S.
Arakawa T., Hara A., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,
Alzawa K., Izawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,
XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Alzawa K., Ashburner M., Batalov S., Casavant T.,
XA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
XA Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,
XA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Xachiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
All D., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
All D., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Androne P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,
XA Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
XA Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Xa Wanshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO08049; BAB25429.1; -.
EMBL, BC019465; AAH19465.1; -.
HSSP; P05451; 1QDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50041; C_TYPE LECTIN 2; 1.
SEQUENCE 157 AA; 18398 MW; F3981722BBD83968 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AA
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                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1914959; 2010002115Rik.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
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PRINTS, PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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01-MAR-2003 (TrEMBLrel
2010002L15Rik protein.
2010002L15RIK.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
    REG-like protein splice variant 2.
                                                                                                                                                                                                                                                                                                                           Local Similarity 55.9
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                             Homo sapiens (Human)
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les 42, Conserva
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121 VCKFK 125
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                                                                                                                                       SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=9606;
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SEQUENCE
                                                                                                                                                                                                                                                                                                          Query Match
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Q8C6F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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                                                                                                                                                                                                                                                                                                                                                                           1 MAYKGVRLLLLLSWVAGPEVLSD-ILRPSCAPGWFYYRSHCYGYPRKLRNWSHAELECOS
                                                                                                                                                                                                                                                                                                                                                 1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                  Query Match 67.7%; Score 594.5; DB 11; Length 157; Best Local Similarity 65.6%; Pred. No. 1.9e-56; Matches 103; Conservative 25; Mismatches 28; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamazanan M., Heiskala K., Heiskala M., Andersson L.C.;
"RELP, a novel human REG-like protein.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX126671; AAMS5599.1;
InterPro; IPR001304; Lectin C.
InterPro; IPR00390; panoreatis_ac.
Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
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                                      MCD; MCI:1914959; 2010002L15Rik.
InterPro; IRR001304; Lectin_C.
InterPro; IRR001390; Pancreatis_ac.
Pfan; PF00059; lectin_c; 1.
PRINTS; PR01504; CLECT; 1.
SMART; SM0034; CLECT; 1.
SROATS; PS0041; C_TYPE LECTIN_2; 1.
SEQUENCE 157 AA; 18474 MW; FD96F3GCFB989368 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PSS0041, C_TYPE LECTIN 2, 1.
SEQUENCE 113 AA; 12832 MW; A2E9DF1A729C78DA CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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  EMBL; AK008438; BAB25669.1; -.
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(TrEMBLrel. 22,
(TrEMBLrel. 22,
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Matches 101; Conservative
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01-OCT-2002
01-OCT-2002
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08NER7
1D 08NE 01-0
DT 01-0
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Q8NER6
ID Q8NE
AC Q8NE
DT 01-0
DT 01-0
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                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                         1 MASRSMRLLILLISCLAXTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAEVRNLL 60
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EMBL; AK075798; BAC35967.1; -.
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                                                                                                                                                                                                                                                                                                                                                  1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAEL----
                                                                                                                                                                                                                                                                               31; Gaps
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PAWPGLSRAKDQPEPQ------ISFDSGSSV---LPGHYEEKPLWL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 ------ECQSYGNGAHLASILSLKEASTIAEYISGYQRSQPIWI 94
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                                                                                                                                                                                                     35.0%; Score 307.5; DB 4; Length 134; 55.9%; Pred. No. 2e-25; tive 9; Mismatches 9; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.8%; Score 235; DB 11; Length 126; illarity 33.6%; Pred. No. 1.3e-17; Conservative 32; Mismatches 45; Indels
Kamarainen M., Heiskala K., Heiskala M., Andersson L.C.; "RELP, a novel human REG-like protein."; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY126572; AAM95500.1; - SEQUENCE 134 AA; 14993 MW; EOESAD9B96A53EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AA; 14340 MW; 2564F04EA9E63094 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seg
01-MAR-2003 (TrEMBLrel. 23, Last ann
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us-09-525-041-2.rspt

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EMBL; AY091759; AAM22787.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GQAEVWIGLWDKKKDFSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLWNDQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NCPPDWLPMNGLCYKIFDELKAWEDAERFCRKYKPGCHLASFHQYGESLEIAEYISDYHK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang W.J., Huang T.F.;
"A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
acts as a glycoprotein Ib agonist.";
Thromb. Haemost. 86:1077-1086(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGYOR
                                                                                                                                                                                                                                                              MEDLINE=96161481; PubMed=8593494; Nikai T., Suzuki J., Komori Y., Ohkura M., Ohizumi Y., Sugihara H.; "Primary structure of the lectin from the venom of Bitis arietans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-type lectin (Agglucetin-alpha 1 subunit precursor)
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                   Bitis arietans (African puff adder).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Bitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ;
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Yu H., Xiang K., Wang Y., Liu J.;
"Member of C-type lectin family from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.7%; Score 234; DB 13; Length 135; 35.1%; Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                    (puff-adder).";
Biol. Pharm. Bull. 18:1620-1622(1995).
HSSP, P22897, 1E86.
InterPro; 1PR003990; Pancreatis_ac.
InterPro; 1PR003990; Pancreatis_ac.
InterPro; 1PR003991; PROFEMATITAP.
PROMOS; SMART; SM00034; CLECT; 1.
PROSITE; PS00615; CTYPE LECTIN 1; 1.
PROSITE; PS00615; CTYPE LECTIN 2; 1.
SEQUENCE 135 AA; 16158 MW; 3A01248FA884C5B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VCGSKNAFLCQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ECNKROHFLCK 155
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Best Local Similarity
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                                                                                                                                                                                        NCBI_TaxID=8692
                                                                                                                                                                                                                                        SEQUENCE
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65 AHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQ--WQWIDGAMYLYRSWSGKS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR
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Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Lachesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aragon-Ortiz F., Mentele R., Auerswald E.A.; "Amino acid sequence of a lectin-like protein from Lachesis muta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
                                                                                                                                                                                                                                                                                                                                              26.3%; Score 230.5; DB 13; Length 154; 32.7%; Pred. No. 5.2e-17; ive 24; Mismatches 70; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 135;
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                                                                                                                                                                                                                                                                   AGGLUCETIN-ALPHA 1 SUBUNIT
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InterPro; IPR001309; Pancreatis_ac.
Pfam, PF00059; lectin_c; 1.
SMART; SW00034; CLECT; 1.
PROSTITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSTITE; PS00615; C_TYPE_LECTIN_2; 1.
SEQUENCE 135 AA; _16223 MW; DSE9083A065A8F56 CRC64;
                                                                                                                                                                                                                                                                                               SEQUENCE 154 AA; 17317 MW; AA08E518501BECC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 MGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.1%; Score 229; DB 13; 34.4%; Pred. No. 6.4e-17; iive 18; Mismatches 64;
                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                          PROSITE, PSO0615, C TYPE LECTIN 1; 1. PROSITE, PSO041; C TYPE LECTIN 2; 1.
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EMBL; AF540645; AAN23124.1; ...
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Panoreatis_ac.
Plam; PF00059; lectin_C; 1.
PRINTS; PR01504; PNRKEATITSAP.
SWART; SM00034; CLECT; 1.
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MEDLINE=97000492; PubMed=8843577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stenophyrs venom.";
Toxicon 34:763-769(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
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154
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Query Match
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Q90WI7
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SITAIN=CS7BL/6J; TISSUE=Small intestine;

MEDINE=2108566). PubMed=11217851;

MARANA T., HARA A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Matsuda H.A., Ashburner M., Betalov S., Yamanaka I.,

Madota K., Matsuda H.A., Ashburner M., Betalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Betalov S., Casavant T.,

Radota K., Matsuda H.A., Nikaido I., Pesole G., Quackenbush J.,

Rushill P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

H.Vonshiami V., V., Koshida K., Hasegawa Y., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 VDNYQDIWIGLHDPTWGQQPNGGGWEWSNSDVLNYLNWDGDPSTVNRGHCGSLTASSGF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RISCPMGYKAYRSHSYALVMTPKSWFQADLVCQKRPSG-HLVSILSGGEASFVSSLVNGR 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse CDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Rat generating islet-derived, mouse homolog 3 alpha (Fragment)
REG3A.
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25.9%; Score 227.5; DB 11; Length 146;
Best Local Similarity 34.5%; Pred. No. 1e-16;
Matches 48; Conservative 25; Mismatches 57; Indels 9;
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SEQÜENCE 146 AA; 16161 MW; 76D73B81BECC5FB1 CRC64;
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InterPro; IPR001304; Lectin_C.
InterPro; IPR001309; Pancreatis_ac.
Pfam; PP00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; PS000134; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 LTWSSNECNKROHFLCKYR 157
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                                     122 VCESKNAFLCO 132
                                                                                                                                              PRELIMINARY;
  145 ECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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                                                                                                    RESULT 10
Q9CVF4
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RESULT 11

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89 SQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGYQR 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cloning and characterization of C-type lectin-like proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
C-type lectin-like protein 1.

Bungarus fasciatus (Banded krait).

Eukaryota: Metazod; Chordets, Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
Elapidae; Bungarinae; Bungarus.
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Bungarus fasciatus (Banded krait).

Bungarus fasciatus (Banded krait).

Bungarus fasciatus (Bordate; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Blapidae; Bungaruse.

Blapidae; Bungarinae; Bungarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 25.9%; Score 227; DB 13; Length 158; 11 Similarity 33.6%; Pred. No. 1.3e-16; 44; Conservative 22; Mismatches 61; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elapidae snakes.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 158 AA; 18638 MW; ECF85936FA4182B8 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF354271; AAK43585.1; -.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C,
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF354270; AAK43584.1; -. InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00059; lectin c; 1.
PRINTS; PRO0356; ANTIFREZEII.
PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zha H.-G., Zhang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elapidae snakes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8613;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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                                                                                                                                                                                                                                                                      EMBL, AF354772; AAK43586.1; -.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 35:5264-5271(1996)
HSSP; P23807; 1IXX.
                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viperidae, Viperinae, Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ECNKROHFLCK 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=40353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                           70 ILSLKEASTIAEYISGYORSOPIWIGLHDPOKROOWOWIDGAMYLYRSWSGKSMGGNKHC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 IHSREEEAFVGKMASRTLKYTSMWLGLNNPWKECKWEWSDDTRLDYKVWTRR-----PYC 119
                                                                                                                                                                                                                                        89 SQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNK---HCAEMSSNNNFLTWSSN 144
                                                                                                                                                                29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                         10 LLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazza, Chordata, Craniata; Uvennagkistrodon acutus).
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu H., Xiang K., Wang Y., Liu J.,
"Member of C-type lectin family from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AXO91760, AAM2788.1,
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.2%; Score 221.5; DB 13; Length 155; 29.7%; Pred. No. 5e-16; Live 28; Mismatches 65; Indels 11;
                                                                                       25.9%; Score 227; DB 13; Length 158; 32.1%; Pred. No. 1.3e-16; ive 26; Mismatches 59; Indels 4
                                                      18254 MW; 5F0218970DA17453 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 155 AA; 17944 MW; 3E935FF53773AB94 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             155 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                           Best Local Similarity 32.19
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                145 ECNKROHFLCK 155
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                                                        158 AA;
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                    PROSITE;
                                                      SEQUENCE
PROSITE;
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Matches
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Q8JIV8
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01-DEC-2001 (TrEMBLrel. 19, Created)

Q90WI6 ID Q9 AC Q9 DT 01

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89 SQ-PIWIGLHDPOKROOWOWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUBE-become jaland; Zha H.-G., Zhang Y.; "CDNA cloning and characterization of C-type lectin-like proteins from "CDNA cloning and characterization of C-type lectin-like proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
C-type lectin-like protein 1.

Bungarus multicinctus (Many-banded krait).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Elapidae; Bungarinae; Bungarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
ECLV IX/X-BP beta SUBUNIT=CA(2+)-dependent coagulation factor
IX/factor X-binding protein beta subunit.
IX/factor X-binding protein beta subunit.
Eukaryota, Metazoa; Chordeta, Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ;
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Chen Y.L., Tsail.H.;
"Functional and sequence characterization of coagulation factor
IX/factor X-binding protein from the venom of Echis carinatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%; Score 214; DB 13; Length 1 32.1%; Pred. No. 3.3e-15; ive 22; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                   Elapidae snakes.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00059; lectin_c; 1.
SMARY; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 125 AA; 14372 MW; EDFEC2E49686CDD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 AA; 18706 MW; 66B71A29D1048805 CRC64;
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Query Match 24.3%; Score 213; DB 13; Length 125; Best Local Similarity 32.5%; Pred. No. 3.2e-15; Matches 41; Conservative 18; Mismatches 61; Indels 6
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116 GHFVCK 121
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Search completed: December 31, 2003, 09:14:57 Job time : 70 secs

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Title: Perfect score:

Sequence:

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Searched:

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Sequence 1073, Ap
Sequence 1073, Ap
Sequence 1073, Ap
Sequence 1, Appli
Sequence 1075
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Sequence 1075, Ap
Sequence 1075, Ap
Sequence 1071, Ap
Sequence 1074, Ap
Sequence 1072, Ap
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Sequence 1069, Ap
Sequence 2117, Ap
Sequence 1057, Ap
Sequence 1057, Ap
Sequence 1057, Ap
Sequence 1057, Ap
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Sequence 1089,
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILLING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
9 US-09-922-217-1073

10 US-09-833-263-1073

14 US-10-025-380-1073

15 US-09-922-217-1075

10 US-09-922-217-1075

10 US-09-922-217-1074

10 US-09-922-217-1074

10 US-09-922-217-1074

10 US-09-922-217-1074

11 US-09-922-217-1074

12 US-09-922-217-1074

13 US-09-922-217-1074

14 US-10-025-380-1071

15 US-10-25-041-1

16 US-09-922-217-1069

17 US-09-922-217-1069

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2 US-10-255-027-383

3 US-09-922-317-069

3 US-09-922-317-069

3 US-09-922-317-069

3 US-09-922-317-057

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3 US-09-93-38-38-32-1218

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US-09-998-598-2535
US-09-998-598-2535
US-10-046-935-367
US-10-146-502-367
US-10-146-502-2001
US-10-046-935-2001
US-10-146-502-2001
US-10-046-935-1089
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Patent No. US20020076414A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Wing, Yuqiu
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
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MASRSMRLLLLLSCLAKTGV.....LTWSSNECNKRQHFLCKYRP 158
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Sequence 1073, Application US/09833263

Sequence 1073, Application US/09833263

Sequence 1073, Application US/09833263

SERERAL INFORMATION:

APPLICANT: Clapper, John A.

APPLICANT: Stolk, John A.

APPLICANT: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833.263

CURRENT FILING DATE: 2001.04-10

NUMBER OF SEQ ID NOS: 1093

CURRENT FILING DATE: 2001.04-10

SEQ ID NO 1073

LENGTH: 474

TYPE: DNA

TYPE: DNA

GRANISM: Homo sapiens

US-09-833-263-1073
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; TYPE: DNA
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APPLICANT: Heiskala, Marja; TILE OF INVENTION: REG-LIKE PROTEIN
FILE REFERENCE: CDS-261; CURRENT FILING DATE: 2002-09-10; PRIOR APPLICATION NUMBER: 60/276,414; PRIOR APPLICATION NUMBER: 60/276,414; PRIOR FILING DATE: 2002-09-10; NUMBER OF SEQ ID NOS: 45; SOFTWARE: Patentin Version 3.1; SEQ ID 0.1.
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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND METHODS FOR THEIR USE
FILE REFERENCE: 20121-471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 201-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1075
LENGTH: 614
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk John A.
APPLICANT: Stolk John A.
APPLICANT: Wang, Tongtong
APPLICANT: Sinfth, Carcle Lynn
APPLICANT: Smith, Carcle Lynn
APPLICANT: King, Gordon E.
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; ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secritst, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Cateer, Jonathan D.
APPLICANT: Cateer, Darry R.
APPLICANT: Cateer, Darry R.
APPLICANT: Cateer, Darrick
APPLICANT: Stolk, Yasir A. W.
APPLICANT: Cateer, Darrick
APPLICANT: Stolk, Yasir A. W.
APPLICANT: Cateer, Darrick
APPLICANT: Stolk, Yasir A. W.
APPLICANT: Stolk, Y
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Sequence 1075, Application US/09833263

Patent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFREENCE: 21012.1.471C12

CURRENT APPLICATION WUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER: OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1075

LENGTH: 614
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ORGANISM: Homo sapiens
US-09-833-263-1075
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                                                                                     61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1074
LENGTH: 1114
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Ku, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Sinth, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
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CRGANISM: Homo sapiens
US-09-922-217-1074
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     CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stock, John A.
APPLICANT: Stock, John A.
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonatha
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APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yuqiu
APPLICANT: Sith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
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ORGANISM: Homo sapiens
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; Patent No. US20020110547A1
; GENERAL INFORMATION:
    APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
    APPLICANT: Clapper, Jonathan D.
    APPLICANT: Stolk, John A.
    APPLICANT: Stolk, John A.
    APPLICANT: BARGHEN, Madeleine J.
    TITLE OF INVENTION: COMPOUNDS FOR COLON CANCER AND METHODS FOR THEIR USE; ITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1071
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Fatent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Glapper, Jonathan D.
APPLICANT: Maddleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICANTION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FaatSEQ for Windows Version 3.0
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411 AAGAGGCAGCAGTGCCAGTGGATTGATGGGGCCCATGTATCTGTACAGATCCTGGTCTGGC
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                                                                                                    471 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
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Matches:
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TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
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Publication No. US20030158098A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon Specific Gene and Protein

FILE REFERENCE: PF178D2

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: US/09/525,041

CURRENT FILING DATE: 2004-06-04

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: PATCHING DATE: 1995-06-06

SEQ ID NO 1

FROM RELING DATE: 1995-06-06

SEQ ID NO 1

FROM RELING DATE: 1995-06-06
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Matches:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (111)..(587)
US-09-525-041-1
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Best Local Similarity:
Query Match:
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US-10-025-380-1071
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81 GluTyr1leSerGlyTyrGlnArgSerGlnPro1leTrp1leGlyLeuHi8AapProGln 100
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APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Gary R.
APPLICANT: Variet Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT TAILNG DATE: 2002.12.19
CURRENT TAILNG DATE: 2002.11.29
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
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Mismatches:
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Sequence 1071, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Macher: Macheline Joy
APPLICANT: Stolk, John A.
APPLICANT: Mang, Tongtong
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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ORGANISM: Homo sapiens
US-10-025-380-1071
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Best Local Similarity:
Query Match:
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Pred. No.:
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Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 1130
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                                                                                              APPLICANT: Secrific.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Renger, Jonathan D.
APPLICANT: Fanger, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Carter, Jourick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLO,
TITLE OF INVENTION: OF COLO,
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT APPLICATION NUMBER: US/10/025,380
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1074
LENGTH: 1114
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Matches:
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              Sequence 1074, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
                                                             APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Ming, Youiu
APPLICANT: Ming, Youiu
APPLICANT: Ming, Youiu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon B.
APPLICANT: King, AJun
APPLICANT: King, AJun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Glapper, Jonathan D.
APPLICANT: Graper, Gary R.
APPLICANT: Vedvick Thomas S.
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CORGANISM: Homo sapiens
US-10-025-380-1074
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Best Local Similarity:
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US-10-157-031-113

Sequence 113, Application US/10157031

Sequence 113, Application No. US20030108890A1

Sequence 113, Application No. US20030108890A1

SEMENAL INFORMATION:

APPLICANT: Baranova, A. V.

APPLICANT: Kozlov, A. V.

APPLICANT: Lobashev, A. V.

APPLICANT: Lobashev, A. V.

APPLICANT: Krkovskaya, L. L.

TILE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REPERENCE: 2760-103

CURRENT APPLICATION NUMBER: US/10/157,031

CURRENT PILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: PatentIn version 3.1
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Human protein; secretory signal; nutritional source; cytokine; immunity;haemetopoisesis; activin; inhibin; tumour; chemotactic; chemokinetic; thrombolytic; anti-inflammatory; inhibition; stomach cancer cell; ds.
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                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of the open reading frame of a novel human protein comprising a secretory signal (AAV29035), isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activininhibhin regulating activity, chemetactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity.
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                                                                                                                                                                                                                               Human proteins with secretory signal sequences - used to treat immune deficiencies, infections, tumours, and haematopoietic
                   /*tag= a
/product= "human protein comprising secretory
signal"
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Location/Qualifiers
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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated protein. (I) and (II) and (II) and be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) carpersaion, such as colonic cancer. For example, (II) may be used to treat disorders associated with decreased expression by cactivity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally (II) may be used to patients own production of them. Additionally (II) may be used to patients own production of them. Additionally (II) may be used to complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used of restorative therapy. (I) may calso be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The and in an anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (E.G. by enzyme linked immunosorbant assays (ELISA)). AAI28460 to AAI29512 and AAMA4494 to AAM24523 represent invention.
                                                                              420
121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
                                               141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
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immunogenic; gene therapy; vaccine; colonic cancer; ss.
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15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
28-AUG-2000; 2000US-0649811.
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E, Wang T,
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Human colon specific gene cDNA sequence SEQ ID NO:1073
99JP-0201279
15-JUL-1999;
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Pred. No.:
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       other;
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Matches:
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/*tag= a
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       G; 103
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       126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its expression product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                               TSA7005 gene, encoding a polypeptide useful for the diagnosis and treatment of diseases associated with its expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpSerSerAsnGluCyBAsnLyBArgGlnHisPheLeuCyBLySTyrArgPro
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                           Claim 3; Page 23; 25pp; Japanese.
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(SAKA ) OTSUKA PHARM
                                     WPI; 2001-303742/32.
P-PSDB; AAB74934.
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us-09-525-041-2.rng

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101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
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                                                                                                                                                                                                                                                      Human REG-like protein (RELP) cDNA
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878.00
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P-PSDB; AAE29829.
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Pred. No.:
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Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer; tumour; immune response; immunostimulant; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                              Stolk JA;
                                                                                                                                                                                                                                                                                                      New polynucleotide, useful for the preparation of a composition stimulating an immune response against, or treating, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the exemplification of the present invention
                                                                                                                                                                                                                            Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk
Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD;
Skeiky YAW, Fanger GR, Vedvick TS, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 474 BP; 126 A; 116 C; 129 G; 103 T; 0 other;
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03-AUG-2001; 2001US-0922217.
19-DEC-2001; 2001US-0025380.
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                        gene; ss.
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                                                                                          121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
361 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; REG-like protein; RELP; tumour; cancer; therapy; chromosome 1;
                                                                                                                                                                                                                          "Human mature REG-like protein"
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immunoglobulin; cytostatic; Ig agonist; immunoglobulin agonist; cancer;
protein therapy; RELP human Ig derived protein; chromosome 1p12-13.1;
                                                                                                                                                                                                                             181 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCACCACCATAGCA
                                                                                                                      LeuGlyAspllelleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
                                                                                                                                                                                                                                                                                 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCACAG
                                                                             MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                            ATGCCTTCCAGAAGCATGCGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC
                                                                                                                                                                    CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                     LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
                                                                                                                                                                                                                                                                                                                                                                AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
                                                                                                                                                                                                                                                                                                                                                                                           Human REG-like protein (RELP) encoding cDNA SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "REG-like protein (RELP)"
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   Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                  The present sequence encodes a new isolated REG-like protein (RELP) human immunoglobulin (Ig) derived protein. RELP comprises: (a) a human variable and constant region, or (b) an isolated human Ig derived protein or specified portion or variant encoded by a nucleic acid. RELP has cytostatic activity and can be used as an Ig agonist and in protein therapy. The RELP human Ig derived protein or a specified portion or variant can be used for preventing or treating a RELP protein mediated condition, malignant condition and disease condition, e.g. cancer. The nucleic acids can be used in producing RELP Ig derived protein. The human RELP protein of the present invention is located to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG
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                                                                                                             New isolated REG-like protein (RELP) human immunoglobulin derived protein or specified portion or variant, useful for preventing or treating a RELP protein mediated condition or malignant condition,
                                                                                                                                                                                                                                                                                                                                                                                                0 other;
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Matches:
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878.00
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P-PSDB; ABP56022.
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Best Local Similarity:
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81 GluTyr1leSerGlyTyrGlnArgSerGlnPro1leTrp11eGlyLeuHisAspProGln 100

101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly

436 AAGAGGCAGCAGTGGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC

61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla

120

140 495

LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr

496 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT

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158 609

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41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 256 recraregraciticadeaagcreadgaacregrereareceaagregagrereagrer 375

us-09-525-041-2.rng

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141 TrpSerSerAenGluCysAenLysArgGlnHisPheLeuCysLysTyrArgPro
                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                        Human Reg 1-gamma protein cDNA sequence.
                                                                                                                                                                                                                                                                                                                   AAI29510 standard; cDNA; 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-2000; 2000WO-US35596
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                                                                                                      regulation; cell growth; development; tumourogenesis; neurodegeneration;
inhibition; treatment; prevention; neoplasia; metastasis;
neurodegenerative change; Alzheimer's disease; Down's syndrome;
regeneration; pancreatic beta-cells; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human Reg I-gamma protein, which comprises a C-type lectin. The sequence was identified in Incyte clone 1310334. Reg I-gamma protein is involved in regulation of call growth and development. Since the overexpression of reg proteins is associated with tumourogenesis and neurodegeneration, inhibition of human Reg I-gamma expression can be used for treading or preventing neoplasia or metastasis and neurodegenerative changes associated with Alzheimer's disease and other disorders of the central nervous system, e.g. Down's syndrome. Reg I-gamma can also be used in therapeutics to induce regeneration of pancreatic beta-cells in the treatment of diabetes. The products can also be used for exercise correspond to the REG.
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human Reg I-gamma protein - useful for developing products for treating, e.g. diabetes, tumours or neuro-degenerative disease such as Alzheimer's
                                                                                           Human; Reg I-gamma protein; C-type lectin; Incyte clone 1310334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 614 BP; 168 A; 143 C; 171 G; 132 T; 0 other;
                                                                    cDNA encoding a human Reg I-gamma protein.
                                                                                                                                                                                    Location/Qualifiers
136..612
/*tag= a
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ВP
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614
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                                             (first entry)
AAV29156 standard; cDNA;
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                                             21-AUG-1998
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(first entry)

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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have expostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by
                                                                                                                                                                                                                                                                                                                                   Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                       Meagher MJ,
                                                                                                                                                                                                                                                                                                                                   Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 465; 472pp; English
                                                                                                                                                                                                                                                                                                                                   Secrist H,
Jiang Y;
10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
                                                                                                             19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
28-AUG-2000; 2000US-0649811.
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                                                                                                                                                                                                                                                                                                                                   Xu J, Lodes MJ,
King GE, Wang T,
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Length: Matches: Conservative: Mismatches: Indels:

1.6e-86 878.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

Gaps:

US-09-525-041-2 (1-158) x AAV29156 (1-614)

LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT

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99US-0476296

tumour; immune response; immunostimulant; cytostatic; vaccine

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rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (FCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigones in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples and antagonist may also be used as diagnostic agents for detecting the presence of TCAPs in samples and ANIZ49212 represent nucleotide and amino acid sequences
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Sequence 614 BP; 168 A; 143 C; 171 G; 132 T; 0 other;

'n	sednence	ce bl4 BP;	168 A; 143 C;	171 G; 132 T; 0 C	other;	
Be R R R R R	Alignment So Pred. No.: Score: Percent Sim: Best Local & Query Match DB:	cores: ilarity: Similarity:	1.6e-86 878.00 100.004 : 100.004 22	Length: Matches: Conservative: Mismatches: Indels: Gaps:	614 158 0 0 0	
š	US-09-525-041	-2 (1-158) × AAI29510 (1	1-614)		
ò		1 MetAlaSe	rArgSerMetArgL	eubeubeubeuser	erArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal	~
ନ୍ଧ	1	36 Argerro	CAGAAGCATGCGGC	rgcrccrattgcrgage	ATGGCTTCCAGAAGCATGCGGCTGCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC	ä
ò		21 LeuGlyAs	pileileMetArgP	roSerCysAlaProGly	LeuGlyAspilelleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn	4
g	н	96 CTGGGTGA		CCAGCTGTGCTCCTGGA		7
ò		41 CysTyrGl	YTYrPheArgLysL	euArgAsnTrpSerAsp	CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer	9
ପ୍ଧ	0	56 TGCTATGG	TTACTTCAGGAAGC	TGAGGAACTGGTCTGAT	TGCTATGGTTACTTCAGGAAGCTGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT	8
ò		61 TyrGlyAs	inglyAlaHisLeuA	laSerIleLeuSerLeu	rGlyAsnGlyAlaHisLeuAlaSerlleLeuSerLeuLysGluAlaSerThrIleAla	8
đ		316 TACGGAAA		CATCTATCCTGAGTTTA		'n
ð		81 GluTyril	eSerGlyTyrGlnA	rgSerGlnProlleTr	GluTyrIleSerGlyTyrGlnArgSerGlnProlleTylleGlyLeuHisAspProGln	Ħ
අු		376 GAGTACAT	AAGTGGCTATCAGA	GAAGCCAGCCGATATGC	GAGTACATAAGTGGCTATCAGAGAGCCGGATATGGATTGGCCTGCACGACCAGAG	4
ò		101 LysArgGl	nGlnTrpGlnTrpI	leAspGlyAlaMetTyz	LysargGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly	7
ď		436 AAGAGGCA		TTGATGGGCCCATGTAT		4
ò		121 LysSerMe	tGlyGlyAsnLysH	isCysAlaGluMetSer	LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr	14
g	4	96 AAGTCCAT	GGGTGGGAACAAGC	ACTGTGCTGAGATGAGC	AGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTAACT	5
ò		141 TrpSerSe	rAsnGluCysAsnLy	TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysT	CystysTyrArgPro 158	
셤	S.	se TGGAGCAG	SCAACGAATGCAACA	TGGAGCAGCAACGAATGCAACAAGCGCCAACACTTCCTGTGCAAGTACCGACCA	TGCAAGTACCGACCA 609	
READID	SULT 9 233696 ABZ33	696 standard;	l; CDNA; 614 BP			
X & :	ABZ33696	96;				
4 63	30	-JAN-2003 (first	st entry)			
X DE	Human	colon specific	gene cDNA	sequence SEQ ID N	NO:1075.	
2 2	Human;	colon cancer;	er; colon tumour;	ur; immunotherapy;	'; diagnosis; cancer;	

diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; and (6) a method for inhibiting the development of cancer in a patient. (I) have immunostimulant and cytostatic activities and can be used in vaccines. AB232646 to AB233725 and ABPS5331 represent human colon cancer/tumour related sequences used in the exemplification of the present invention.

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The present invention describes compounds (I) for the immunotherapy and

Disclosure, Page 467; 537pp; English.

New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer

WPI; 2003-067548/06.

Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA; Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD; Skeiky YAW, Fanger GR, Vedvick TS, Carter D;

10-APR-2001; 2001US-0833263. 03-AUG-2001; 2001US-0922217. 19-DEC-2001; 2001US-0025380.

(CORI-) CORIXA CORP

09-APR-2002; 2002WO-US11475.

WO200283070-A2

24-OCT-2002

Homo sapiens.

gene; ss.

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316 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 375
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101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
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                                              CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                          247 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGGA
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/note= "5' primer site for PCR amplification
and baculovirus expression"
complement (112..128)
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gene therapy; ss.
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111..587
4.tag= a
/product= mature colon specific protein
complement (111..130)
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/note= "5'
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P-PSDB; AAW12691.
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 The present sequence encodes a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its
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                                                                                                                            TGGAGCAACGAATGCAACAAGCGCCAACAACACTTCCTGTGCAAGTACCGACCA 609
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/product= "TSA7005 protein"
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P-PSDB; AAB74934.
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Pred. No.:
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                                                                                              A cDNA clone (AAT51784) codes for a colon specific protein (AAW12691) that may be useful as a diagnostic marker for colon cancer. It is believed that the presence of active transcription of the colon specific gene in non-colon cells of a host is indicative of colon cancer metastases. The cDNA, deposited as ATCC 97129, was isolated from a human colon cancer cDNA library. It can be used to design diagnostic probes, to produce recombinant colon specific protein in transformed host cells, in the gene therapy of patients having need of a colon specific gene protein, or to design antisense constructs useful for treatment of colon cancer.
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             colon specific gene - used to develop prods. for and treatment of colon disorders, partic. colon
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                                                                     Claim 4; Page 51-52; 64pp; English
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GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAspProGln 100
                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human colon specific gene. The nucleic acid sequence can be used to develop products for the diagnosis of a disorder of the colon, e.g. colon cancer or metastases. The products can also be used to screen for agonists or antagonists for the polypeptides. The antagonists may be used to treat colon cancer, since they interact with the function of colon specific polypeptides to inhibit functions which are necessary for the viability of colon cancer cells. The products can also be used for the production of antibodies and for the identification of receptors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGTGATATCATCATGAGACCCAGCTGTGCTCTCGGATGGTTTTACCACAAGTCCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated human colon specific gene - used to develop products for the diagnosis and treatment of disorders of the colon, e.g. colon
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/note= "colon specific gene"
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                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           cancer and metastases
                                                                                                                                                                                                                                                                         WPI; 1999-130432/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                           sapiens
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Stolk JA;

Claim 2; Page 464; 472pp; English

US-09-525-041-2 (1-158) x AAA62951 (1-1114)

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121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
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                                                                                                                                        231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT
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                                                                                                                                                               TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                 411 AAGAGGCAGCAGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC
                                                                                                                                                                                                                                                                                                                                    471 AAGTCCATGGGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAAACT
             MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                               41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                                                                                                                                                                     Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon specific gene cDNA sequence #1.
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10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-057551.
29-UJN-2000; 2000US-069448.
28-AUG-2000; 2000US-0649481.
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King GE, Wang T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human colon specific polypeptides and polynucleotides for diagnosis and treatment of colon cancer, for screening compounds which interact with polypeptide, for synthesis of DNA and manufacture of DNA
              AAGAGGAGCAGCAGCAGCAGCAGGATTGATTGAGGGCCCATGTATCTGTACAGATCCTGGTCTTGCC
LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
                                                  LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
                                                               AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
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/product= "Colon specific protein"
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1111..587
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P-PSDB; AAB12900.
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AAI29509;

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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) cypresion, so that the cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to complementary sequences may also be used as the protein. (II) and its complementary sequences may also be used as by probes in diagnostic complementary sequences may also be used as by probes in diagnostic complementary sequences may also be used as using the resence of similar nucleic acids in samples, and complementary sequences may also be used of restorative therapy. (I) may calso be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to down regulate (TCAP expression and activity. The anti-(I) antibodies may also be used as adiagnostic agents for detecting the presence of TCAPs in samples cand Amazwayyy to Amazyayy (ELSA). AAI28460 to AAI29512 cond and adaption of the prosence of the presence of the 
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Seguence 1114 BP; 288 A; 291 C; 262 G; 273 T; 0 other;

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470
                                                                                                  171 CTGGGTGATATCATCATGAGACCCAGCTGTGTCTCCTGGATGGTTTTACCACAAGTCCAAT 230
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AAI29509 standard; cDNA; 1114 BP

RESULT 15 AAI29509 ID AAI293

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The present invention describes colon tumour associated proteins (I) and the polymucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the conting of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may calso be used as antigates in the production of antibodies and antigates in the production of antibodies and activity. Anti-(I) antibodies and antagonists may also be used to down regulate to TCAP expression and activity. The anti-(I) antibodies may also be used as addiagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used as addiagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents in antibodies.
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                                                                                                                                                       Human; immunotherapy; diagnosis; colon cancer; colon tumour;
immunogenic; gene therapy; vaccine; colonic cancer; ss.
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                                                                                                          Human colon specific gene cDNA sequence #2
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King GE, Wang T, Jiang Y;
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10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0572551.
29-JUN-2000; 2000US-069481.
28-AUG-2000; 2000US-0649811.
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121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
                     291 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACATAGGA 350
                                                                                                                                                                                           81 GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAspProGln 100
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Search completed: December 31, 2003, 09:29:07 Job time : 254 secs

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BD167401 Method of
AF254415 Homo sapi
AX136670 Homo sapi
AX13670 Homo sapi
AX131380 Sequence
AX1351470 Sequence
AX1351470 Sequence
BD108868 EST and e
BC019465 Mus muscu
AX179034 Sequence
AX179115 Sequence
AX179115 Sequence
AX379125 Sequence
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BD062766 Human pro
E52141 TSA7005 gen
AX57651 Sequence
AX193508 Sequence
AX193508 Sequence
AX100599 Sequence
AX100599 Sequence
AX10599 Sequence
AX193504 Sequence
AX193504 Sequence
AX193505 Sequence
BD062775 Human pro
AX193502 Sequence
BD062775 Human pro
AX193502 Sequence
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cgn2_1/USPTO spool_p/USO9525041/runat_31122003_091149_11864/app_query.fasta_1.327
-Q=/Cgn2_1/USPTO spool_p/USO9525041/runat_31122003_091149_11864/app_query.fasta_1.327
-DB=GGnEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1_-LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosmm62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=sext -HEAPSIZE=500 -MINLEN=0 -WAXIEN=2000000000
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-NO WMAP -LARGEOUERY -NEG_SCORES=0 -WAIT -SOSPELOCK=100 -LONGLOG
-NO WMAP -LARGEOUERY -NEG_SCORES=0 -WAIT -SOSPELOCK=100 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                     December 31, 2003, 09:16:53 ; Search time 2146 Seconds (without alignments) 3011.986 Million cell updates/sec
                                                                                                                                                                                                                                  MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                      5777422
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Perfect score:
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Homo sapiens
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Best Local Similarity:
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Human proteins having secretory signal sequences and DNAs encoding
these proteins.
              PAT 15-AUG-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                              Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.
Compounds for immunotherapy and diagnosis of colon cancer and methods for their use
Patent: WO 0149-16-A 1073 12-JUL-2001,
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TrpSerSerAanGluCyaAanLyaArgGlnHisPheLeuCyaLyaTyrArgFro 158
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Matches:
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        474 bp Di
Sequence 1073 from Patent W00149716.
AX193506
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                                                   AX193506.1 GI:15211446
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Query Match:
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 47).
Kato,S., Sekine,S., Kimura,T. and Kobayashi,M.
Human proteins having secretory signal sequences and DNAs encoding
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SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
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SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
SAGAMI CHEMICAL RESEARCH
SAGAMI CHEMICAL RESEARCH
SP 22-MAY-2001
PP 12-SEP-199-109 1998513509
PR 13-SEP-1996 UP 8/243060
PI SEISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, MIDORI KOBAYASHI PC
C12N15/12, C07K14/47, C12N15/62
CC Strandedness: Double;
CC Topology: Linear;
FH Key
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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/organism="Homo sapiens"
/orze="genomic DNA"
/db xref="taxon:9606"
a _116 c 129 g 103
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GI:22608369
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878.00
100.00%
100.00%
                 JP 2001506484-A/3.
Homo sapiens (human)
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RESULT 3

ACCESSION

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PAT 23-NOV-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for detecting reg-like protein and nucleic acids coding therefor
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Ortho-Clinical Diagnostice, Inc. (US)
Location/Qualifiers
1. .47
/organism="Homo saplens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
127 a 116 c 130 g 104 t
                                                             DNA
                                                            AX537651 477 bp
Sequence 1 from Patent EP1241269,
AX537651 GI:25269611
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PN JP 2001025389-A/1
PN JP 2001025389-A/1
PD 30-JAN-2001
PP 15-JUL-1999 JP 1999201279
PR 15-JUL-1999 JP 1999201279
PR TSUYOSHI GOGNARA, MIKIO SUZUKI, KOICHI OZAKI
PC C12N15/09, CO7K14/47, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10//AG1K31/00,
PC A61K38/00, A61K48/00, C12P21/02, C12N15/00, C12N5/00, A61K37/02 CC
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1. 474

/organism='Unknown'.

Location/Qualifiers
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Ogawara,T., Suzuki,M. and Ozaki,K.
TSA7005 gene
Patent: JP 2001025389-A 1 30-JAN-2001,
OTSUKA PHARMACEUT CO LTD
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E52141.1 GI:18629624
JP 2001025389-A/1.
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Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
Patent: WO 0149716-A 1075 12-JUL-2001;
CORIXA CORPORATION (US)
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1 (bases 1 to 1060)
Cgawara, T., Suzuki, M. and Ozaki, K.
TSA7005 gene
Fatent: JP 201025389-A 2 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
OS UNKNOWN
PN JP 200105389-A/2
PD 30-JAN-2001
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                                                                   Location/Qualifiers
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TSA7005 gene.
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E52142.1 GI:18629625
JP 2001025389-A/2.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 1075 from Patent W00149716.
AX193508 GI:15211448
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Bandman,O. and Goli,S.K.
Human Reg protein
Patent: US 5837841-A 2 17-NOV-1998;
Location/Qualifiers
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Sequence 2 from patent US 5837841.
AR058965
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PF 15-JUL-1999 JP 1999201279
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TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00,A61K31/00
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                                                                                                                                    others
                                                              Location/Qualifiers
(67)..(540).
Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
a _ 278 c 247 g 264 t 2
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Matches:
Conservative:
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1 (bases 1 to 1114)
Soppet, D.N., Li, Y. and Dillon, P.J.
Colon specific gene and protein
Patent: US S861494-A 1 19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR030953 1114 bp
Sequence 1 from patent US 5861494.
AR030953
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Soppet, D.R., Li, Y. and Dillon, P.J.
Colon specific gene and protein
Patent: US 6080722-A 1 27-UNM-2000;
Location/Qualifiers
1. 1114
Organism="unknown"
Cg88 a 291 c 262 g 273 t
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Sequence 1 from patent US 6080722.
AR100599
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2 4 4 6 6 7	Oy 61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla 80 291 TACGGAACGCACCTCGCATCTGCTGAGTTTAAAGGAAGCCAGCACCATAGCA 350 Qy 81 GluTyrIleSerGlyTyrGlnArgSerGlnProlleTrpIleGlyLeuHisAspProGln 100 351 GAGTACATAAGGGCTATCAGAGAAGCCAGCCGATAGGATTGGCTGCAGCCCCACAG 410 Qy 101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120	121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnAsnPheLeuThr 121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnAsnPheLeuThr 471 AaGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT 141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158	RESULT 11 AX193507 LOCUS LOCUS DEFINITION Sequence 1074 from Patent W00149716. ACCESSION AX193507 VERSION AX193507.1 GI:15211447 KEYWORDS SOURCE Home sapiens (human) ORGANISM Home sapiens (human) ORGANISM Home sapiens (homes appleans (hom	REPERENCE 1 Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo. REPERENCE 1 AUTHORS Xu,J.; Lodes,M.U.; Secrist,H., Benson,D.R., Meagher,M.J.; Stolk,J.A., King,G.E., Wang,T. and Jiang,Y. TITLE Compounds for immunotherapy and diagnosis of colon cancer and methods for their use JOURNAL Patent: WO 0149716-A 1074 12-JUL-2001; CORIXA CORPORATION (US)	FEATURES Location/Qualifiers 1. 1114 Source 1. 000 sapiens" /organism="Homon sapiens" /mol_type="9enomic DNA" /mol_type="9enomic DNA" /db_xref="taxon:9606" ORIGIN ORIGIN	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Decrept Matches: Best Local Similarity: 100.00\$ Mismatches: Ouery Match: 6 Gaps: OS-09-525-041-2 (1-158) x AX193507 (1-1114)	Oy 1 MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20
Query Match: 100.00\$ Indels: 0 DB: 6 Gaps: 0 US-09-525-041-2 (1-158) x AR100599 (1-1114) QY 1 MetalaSerArgSerMetargLeuLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyval 20 Phill 1111 ATGGCTTCCAGAAGCAGCTGCTGCTGTTGTCTGAGCTGCTGGCCAAACAGGGGGTC 170 QY 21 LeuGlyAspIleIlMetargProSerCysAlaProGGCTGCTGGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGT	41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60 [11] [11] [11] [11] [11] [11] [11] [11	Db 351 GAGTACATAGGGCTATCAGAGAGCCGGCTGGCTGCTGCTCTCTCT	141 TrpSerSerAanGluCysAanLysArgGlnHisPheLeuCysLysTyrArgPro 158	VERSION AX193504.1 GI:15211444 KEYWORDS AX193504.1 GI:15211444 KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Xu,J., Lodes,M.J., Secrist, H., Benson, D.R., Meadher, M.J.,	Stolk, J.A. Compounds methods fo Patent: W CORIXA COF	/mol_type="genomic /dol_type="genomic /dol_xref="taxon:96	isl Similarity: 100.00\$ Mismatches: ttch: 100.00\$ Indels: 6 Gaps: 6-041-2 (1-158) x AX193504 (1-1114)

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Homo sapiens
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1130)
Hartupee, J. C., Zhang, H., Bonaldo, M.F., Soaree, M.B. and
Dieckgraefe, B.K.
Isolation and characterization of a cDNA encoding a novel member of the human regenerating protein family: Reg IV
Biochim. Blophys. Acta 1518 (3), 287-293 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-AUG-2000) Gastroenterology, Washington University School of Medicine, 660 S. Euclid Ave., Campus Box 8124, St. Louis, MO 63110, USA
                                                                 303 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 362
                                                                                                                                                                        LysSerMetGlyGlyAgnLysHisCysAlaGluMetSerSerAgnAgnAgnPheLeuThr
                                                                                                                                  483 AAGTCCATGGGTGGGAACAAGCACTGTGTGTGTGAGCTCCAATAACAACTTTTTAACT
                 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLygGluAlaSerThrIleAla
                                                                                                                     LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
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Dieckgraefe, B.K., Hartupee, J.C., Zhang, H., Soares, M.B. and
Bonaldo, M.F.
Direct Submission
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Homo sapiens regenerating gene type IV mRNA, complete cds.
AY007243
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/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                           GluTyrileSerGlyTyrGlnArgSerGlnProileTrpileGlyLeuHisAspProGln 100
                                                                                                                                                                      351 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 410
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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In silico screening for phenotype-associated expressed sequences Patent: WO 02103028-A 113 27-DEC-2002;
Biomedical Center (RU)
Location/Qualifiers
1. .1130
61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                       CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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Seguence 113 from Patent W002103028.
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Homowaptota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

E. (Dasses 1 to 1152)

I. (Dasses 1 to 1152)

Kato, S., Sekine, S., Kimura, T. and Kobayashi, M. Human proteins having secretory signal sequences and DNAs encoding these proteins

L. Patent. JP 2001506444-A 12 22-MAY-2001,

SAGAMI CHENICAL RESEARCH CENTER, PROTEGENE INC

OS Homo sapiens (human)

PN 192-MAY-2001

PP 12-SEP-1997 JP 1998513509

PR 11-SEP-1997 JP 1998513509

PR 11-SEP-1997 JP 1998513509

PR 11-SEP-1996 JP 8/243060

PI SEISHI KAYO, SHINGO SEKINE, TOMOKO KIMURA, MIDORI KOBAYASHI PC

CL2N15/12, CO7KL4/47, C12N15/62

CC Strandedness: Double;

CC Tropology: Linear,

FR Key

FT CDS
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                                                                                                                                                                                                           101 LysargGinGinTrpGinTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
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                                                                                                          267 IGCTATGGTTACTTCAGGAAGCTGAAGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 326
                                                                                                                                                             DNA linear PAT 27-AUG-200 signal sequences and DNAs encoding
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                                                                                                                                            61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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a _298 c 275 g 283
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JP 2001506484-A/12.
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                                243 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 302
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                              303 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA
                                                                                             21 LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
                                                                                                                                                             CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                             61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                                                                                                         AAGAGGCAGCAGTGGCATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGGTCCAATAACAACTTTTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
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Conservative:
Mismatches:
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AX193505
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US-09-525-041-2 (1-158) x AY007243 (1-1130).
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Homo sapiens
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AX193505
LOCUS
DEFINITION
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1 MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20
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Search completed: December 31, 2003, 10:05:08 Job time : 2151 secs

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Query Match 100.
Best Local Similarity 100.
Matches 158; Conservative
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138, App
781, App
861, App
1200, Ap
                                                                                                                                                                December 31, 2003, 09:15:03 ; Search time 72 Seconds (without alignments) 440.296 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-09-922-217-1071
US-09-922-217-1079
US-09-922-217-1079
US-09-932-217-1079
US-09-833-263-1077
US-09-833-263-1077
US-09-833-263-1077
US-09-833-263-1079
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US-09-625-027-138
US-10-295-027-138
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 1070, Ap Sequence 1077, Ap Sequence 1078, Ap Sequence 1080, Ap Sequence 2, Appli Sequence 24, App Sequence 347, App Sequence 753, App Sequence 753, App Sequence 110, App Sequence 109, App Sequence 1182, App Sequence 109, App Sequence 1013, App Sequence 11, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 65, Appli Sequence 452, App Sequence 452, App Sequence 452, App Sequence 452, App Sequence 452, App
US-09-978-697-452
US-09-978-192A-452
US-09-999-832A-452
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ALIGNMENTS

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Gaps
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APPLICANT: Lodes, Michael J.
APPLICANT: Becrist, Heather
APPLICANT: Becrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Wang, Yugiu
APPLICANT: Wing, Yugiu
APPLICANT: Wing, Carole Lynn
APPLICANT: Wing, Ajun
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Wing, Ajun
APP
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100.0%; Pred. No. 7.6e-86;
Live 0; Mismatches 0; Indels
Sequence 1070, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
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121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                     NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                          CURRENT APPLICATION NUMBER: US/09/922,217 CURRENT FILING DATE: 2001-08-03
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Patent No. US20020076414A1
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APPLICANT: Lodes Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Maegher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Mang, Tongtong
                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-1078
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US-09-922-217-1079
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPERBACE: 210121.471013
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1077
LENGTH: 158
TAND.
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Patent No. US2002007441A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                   Sequence 1077, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                      Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
Maagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
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Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yugiu
Smith, Carole Lynn
King, Gordon E.
Wang, Aljun
Clapper, Jonathan D.
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US-09-922-217-1077
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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APPLICANT: Sinith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Gapper, Jonathan D.
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 158;
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Query Match
Best Local Similarity
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US-09-833-263-1070

; Sequence 1070, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Anjun
; APPLICANT: Madeleine J.
; APPLICANT: Maegher, Jonathan D.
; APPLICANT: Maegher, Madeleine J.
; APPLICANT: Maegher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE;
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FESTESEQ for Windows Version 3.0
; SEQ ID NO 1070
; LENGTH: 158
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE 210121.1471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
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121 KSMGGNKHCAEMSSNNNPLTWSSNECNKRQHPLCKYRP 158
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                    RESULT 5
US-09-922-217-1080
; Sequence 1080, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Macapher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
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Smith, Carole Lynn
King, Gordon E.
Wang, Aijun
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US-09-922-217-1080
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ORGANISM: Homo sapiens
US-09-833-263-1070
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Best Local Similarity
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APPLICANT:
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Aijun APPLICANT: Clapper, Jonathan D. APPLICANT: Clapper, John A. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Meagher, Madelaine J. IITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121/17/17/21/2 CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1077
LENGTH: 158
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       Length 158;
                                                                       Indels
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Query Match 100.0%; Score 878; DB 10; Best Local Similarity 100.0%; Pred. No. 7.6e-86; Matches 158; Conservative 0; Mismatches 0;
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Patent No. US20020110547A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-833-263-1077
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RESULT 12
US-10-295-027-138
                                                                                       SEQ ID NO 1080
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Sequence 1079, Application US/09833263

Sequence 1079, Application US/09833263

Sequence 1079, Application US/09833263

SEQUENCE INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

APPLICANT: Maddleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: UNMER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SEQ ID NO 1079

LENGTH: 158
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; Sequence 1080, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
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                                                                                                                                                                                                                                                  1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0
                                                                                                               Length 158;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                       121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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                                                                                                          ; Score 878; DB 10;
; Pred. No. 7.6e-86;
0; Mismatches 0;
                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 158; Conservative 0
              TYPE: PRT
CRGANISM: Homo sapiens
US-09-833-263-1078
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US-09-833-263-1079
LENGTH: 158
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWWDGAMYLYRSWSG 120
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| Publication No. US20030158098A1
| GENERAL INFORMATION:
| APPLICANT: Soppet et al.
| TITLE OF INVENTION: Colon Specific Gene and Protein
| FILE REFERENCE: PP178D2
| CURRENT APPLICATION NUMBER: US/09/525,041
| PRIOR APPLICATION NUMBER: US 09/162,508
| PRIOR FILING DATE: 1998-09-29
| PRIOR FILING DATE: 1998-06-29
| PRIOR FILING DATE: 1998-06-06
| NUMBER OF SEQ ID NOS: 6
| NUMBER OF SEQ ID NOS: 6
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100.0%; Pred. No. 7.6e-86;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/833,263
UNRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FASTSEQ for Windows Version 3.0
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 158; Conservative
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ORGANISM: Homo sapiens
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWUDGAMYLYRSWSG 120
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APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-01250002
CURRENT FILING DATE: 2002-11-13
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-02-01
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APPLICANT: Murray, Richard
APPLICANT: Mateon, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-0125600US
CURRENT APPLICATION NUMBER: US/10/295,027
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsberg, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Manne, Diagram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-295-027-781
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                                                                                                                                              APPLICANT: Hevezi, Pater A.
APPLICANT: Hevezi, Pater A.
APPLICANT: Hevezi, Richard
APPLICANT: Murray, Richard
APPLICANT: Mack, David H.
APPLICANT: Wasen, Susan R.
APPLICANT: Wasen, Susan R.
APPLICANT: Eos Biotecchnology, Inc.
APPLICANT: Bos Biotecchnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: WHORER: US, 10/295, 027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US, 60/350, 666
PRIOR PELING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US, 60/340, 376
PRIOR PELING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US, 60/340, 376
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2002-01-00
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2003-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Afer, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Watson, Susan R.
                Ginsberg, Wendy M
                                                                                     Glynne, Richard
Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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US-10-295-027-781
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR PILING DATE: 2001-11-24

PRIOR PELING DATE: 2001-12-14

PRIOR PELING DATE: 2002-12-14

PRIOR PELING DATE: 2002-01-08

PRIOR PILING DATE: 2002-01-10

PRIOR PILING DATE: 2002-01-10

PRIOR PILING DATE: 2002-02-08

PRIOR APPLICATION NUMBER: US 60/356,714

PRIOR PILING DATE: 2002-02-13

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1386
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Matches 158; Conservative
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                                                                                                  PRIOR FILING DATE: 2001-11-15
PRIOR PLICATION NUMBER: US 60/335,394
PRIOR PELIANG DATE: 2001-11-15
PRIOR PELIANG DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-11-29
PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2001-12-14
PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-02-01
PRIOR PLING DATE: 2002-02-02
PRIOR PLING DATE: 2002-02-02
PRIOR PRIOR PLING DATE: 2002-02-13
PRIOR PLING DATE: 2002-02-13
PRIOR PLING DATE: 2002-02-13
PRIOR PLING DATE: 2002-02-13
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PRIOR PLING DATE: 2002-02-13
PRIOR PLING DATE: 2022-02-13
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APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotecchnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer.
FILE REPRENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
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PRIOR PILING DATE: 2001-11-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 878;
100.0%; Pred. No. 7
                                               999'058/09
                                                                                FILING DATE: 2001-11-13
APPLICATION NUMBER: US 60/335,394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Afar, Daniel
APPLICANT: Aziz, Nateasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
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Best Local Similarity 100.
Matches 158; Conservative
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ORGANISM: Homo sapiens
US-10-295-027-861
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